

SEQUENCE LISTING

<110> Hermon-Taylor, John
 Doran, Tim
 Millar, Douglas
 Tizard, Mark
 Loughlin, Mark
 Sumar, Nazira

<120> NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES IN PATHOGENIC
 MYCOBACTERIA AND THEIR USE AS DIAGNOSTICS, VACCINES AND
 TARGETS FOR CHEMOTHERAPY

<130> 117-260

<140> 09/091,538

<141> 1998-06-19

<150> PCT/GB96/03221

<151> 1996-12-23

<150> GB 9526178.0

<151> 1995-12-21

<160> 41

<170> PatentIn Ver. 2.0

<210> 1

<211> 674

<212> DNA

<213> Mycobacterium

<400> 1
 gatccaacta aacccgatgg aaccccgcgc aaactattgg acgtctccgc gctacgcagt 60
 tgggttggcg cccgcgaatc gcactgaaag agggcatcga tgcaacgggtg tcgtggtacc 120
 gcacaaatgc cgatgccgtg aggaggtaaa gctgcggggc ggccgatgtt atccctccgg 180
 cccgacgggt agggcgacct gccatcgagt ggtacggcag tcgcctggcc ggcgaggcgc 240
 atggcctatg tgagtatccc atagcctggc ttggctcgcc cctacgcatt atcagttgac 300
 cgctttcgcg ccacgtcgca ggcttgcggc agcateccgt tcaggctctcc tcatgggtccg 360
 gtgtggcacg accacgcaag ctcgaaaccga ctcgtttccc aatttcgcat gctaatatcg 420
 ctcgatggat tttttgcgca acgccggctt gatggctcgt aacgttagca ccgagatgct 480
 gcgccactcc gaacgaaagc gcctattagt aaaccaagtc gaagcatacg gagtcaacgt 540
 tgttattgat gtcggtgcta actccggcca gttcggtagc gctttgcgtc gtgcaggatt 600
 caagagccgt atcgtttccct ttgaacctct ttcggggcca tttgcgcaac taacgcgcaa 660
 gtcggcatcg gatc 674

<210> 2

<211> 674

<212> DNA
 <213> Mycobacterium

<400> 2
 gatccgatgc cgacttgcg gttagttgcg caaatggccc cgaaagaggt tcaaaggaaa 60
 cgatacggct cttgaatcct gcacgacgca aagcgctacc gaactggccg gagttagcac 120
 cgacatcaat aacaacggtg actccgtatg cttcgacttg gtttactaat aggcgctttc 180
 gttcggagtg ggcgagcatc tcggtgctaa cgttacgagc catcaagccg gcgttgcgca 240
 aaaaatccat cgagcgatat tagcatgcga aattgggaaa cgagtcgggt cgagcttgcg 300
 tggtcgtgcc acaccggacc atgaggagac ctgaacggga tgctgccgca agcctgcgac 360
 gtggcgcgaa agcgggtcaac tgataatgcg tagggcgag ccaagccagg ctatgggata 420
 ctcacatagg ccatgcgcct cgccggccag ggcactgccg taccactcga tggcaggtcg 480
 ccctaccctg ccggccggag ggataacatc ggccggcccg cagctttacc tcctcacggc 540
 atcggcattt gtgcggtacc acgacaccgt tgcatcgatg ccctctttca gtgcgattcg 600
 cgggcgccaa cccaactgcg tagcgcgag acgtccaata gtttgcgcg gggtccatcg 660
 ggtttagttg gatac 674

<210> 3
 <211> 7995
 <212> DNA
 <213> Mycobacterium

<400> 3
 gaattctggg ttggagacga cgtcgaactc ctggtcggtc ttgcttcgaa tgatcgctgt 60
 gatctggtcg gcggtgccga caggaaccgt cgacttgctg acgatcacct tgtaccggtc 120
 gatgtatgac ccaatgtcgt ccgcaaccga gaagacgtac gtcagggtccg ccgccccgct 180
 ttcaaccatg ggctgcggga cggcgatgaa aatgacgtcc gcgtgctcga ttccgcgttg 240
 ccggtcgggtg gtgaagtcaa tcagcccgtt ctcacgggtc ctcgcaatca actcccaacc 300
 cgggctcgaa aatcgggaca ctgcctgcga ggagcaaata gatcttggtc tgatcgatat 360
 cgacacagac gacatcggtg ccgctatccg cgagacaggc gcccgtagcg aggcctacat 420
 agcctgatcc gaccaccgaa attttcaaga tgacccttc aagtccccga tcgggtcgacg 480
 accatactgc cgcaactctg taccctccgt gggtaattcg catgtcgcgt tcgtaaggag 540
 cagccagcga gtcggggacg ttcggtgaga gagtcgcagg actacgaggt tgccgggtgcg 600
 atacatcaca gtgttgctc tgtcggcaac gatgcagcaa gaaccacgg ggcagccctg 660
 aactgcgcgc atgaccggtc cttgtcctgg cacctttgat cggccaccgc ttccatgcga 720
 acatgaccgg aatccatagc gcgtggtcaa gcagcgggga ggtagacgtc ggtgtcatct 780

gctccaaccg tgtcgggtgat 'aacgatttcg ctgaacgata tcgagggatt gaaaagcacc 840
 gtggagagcg ttcgcgcgca gcgctatggg gggcgaatcg agcacatcgt catcgacggt 900
 ggatcggggc acgccgtcgt ggagtatctg tccggcgatc ctggctttgc atattggcaa 960
 tctcagcccg acaacgggag atatgacgcg atgaatcagg gcattgccca ttcgtcgggc 1020
 gacctgttgt ggtttatgca ctccacggat cgtttctccg atccagatgc agtcgcttcc 1080
 gtggtggagg cgctctcggg gcatggacca gtacgtgatt tgtgggggta cgggaaaaac 1140
 aacctgtcgt gactcgacgg caaaccactt ttccctcggc cgtacggcta tatgccgttt 1200
 aagatgcgga aatttctgct cggcgcgacg gttgcgcata aggcgacatt cttcggcgcg 1260
 tcgctggtag ccaagtggg cggttacgat cttgattttg gactcgaggc ggaccagctg 1320
 ttcactacc gtgccgcaact aatacggcct cccgtcacga tcgaccgcgt ggtttgcgac 1380
 ttgatgtca cgggacctgg ttcaaccag cccatccgtg agcactatcg gacctgcgg 1440
 cggctctggg acctgcatgg cgactaccg ctgggtgggc gcagagtgtc gtgggcttac 1500
 ttgcgtgtga aggagtactt gattcggggc gacctggcgc cattcaacgc ggtaaagtcc 1560
 ttgcgagcga agttcgccag agcttcgcgg aagcaaaatt catagaaacc aacttctact 1620
 gcctgacctg agcagcgccg aggcgcgcag cgcgatcagt gcgacctgaa cggccaggcg 1680
 gaaagcgcca ccgatccgg caccgagtgc ctgacgcttc ggatcccttg caccacaacg 1740
 agagtgagag cgccatgatg aggaaatata ggctggcgcg agtcaacgcc ggagtgacaa 1800
 aagtgagaac ccggtgaagc gagcgcttat aacagggatc acggggcagg atggttccca 1860
 cctcgccgag ctactactga gcaagggata cgagggtcac gggtcgttc gtcgagcttc 1920
 gacgtttaac acgtcgcgga tcgatcacct ctacgttgac ccacaccaac cgggcgcgcg 1980
 cttgttcttg cactatgcag acctcactga cggcaccgg ttggtgacct tgctcagcag 2040
 tctcgacctg gatgaggtct acaacctcgc agcgcagtcc catgtgcgcg tcagctttga 2100
 cgagccagtg cataccggag acaccaccgg catgggatcg atccgacttc tggaaagcagt 2160
 ccgcctttct cgggtggact gccggttcta tcaggcttcc tcgtcggaga tggtcggcgc 2220
 atctccgcca ccgcagaacg aatcgacgcc gttctatccc cgttcgcat acggcgcggc 2280
 caaggtcttc tcgtactgga cgactcgcaa ctatcgagag gcgtacggat tattcgcagt 2340
 gaatggcacc ttgttcaacc atgagtcccc cggcgcgcgc gagactttcg tgacctgaaa 2400
 gatcacgcgt gccgtggcgc gcatccgagc tggcgtccaa tcggaggtct atatgggcaa 2460
 cctcgatgcg atccgcgact ggggctacgc gcccgaaat gtcgagggga tgtggaggat 2520
 gttgcaagcg cctgaacctg atgactacgt cctggcgaca gggcgtgggt acaccgtacg 2580
 tgagttcgct caagctgctt ttgacctgt cgggctcgac tggcaaaagc gcgtcaagtt 2640

tgacgaccgc tatttgcgtc ccaccgaggt cgattcgcta gtaggagatg ccgacaaggc 2700
 ggcccagtca ctcggtgga aagcttcggt tcatactggt gaactcgcgc gcatcatggt 2760
 ggacgcgga acgcccgt tggagtgcga tggcacacca tggatcgaca cgccgatgtt 2820
 gcctggttg ggagagtaa gttgacgact acacctgggc ctctggaccg cgcaacgccc 2880
 gtgtatatcg ccggtcatcg ggggctggtc ggctcagcgc tcgtacgtag atttgaggcc 2940
 gaggggttca ccaatctcat tgtgcatca cgcgatgaga ttgatctgac ggaccgagcc 3000
 gcaacgtttg attttgtgtc tgagacaaga ccacaggtga tcatcgatgc ggccgcacgg 3060
 gtcggcgga tcatggcgaa taacacctat ccgcggact tcttgtccga aaacctccga 3120
 atccagacca atttgctcga cgcagctgtc gccgtgcgtg tgccgcggct ccttttctc 3180
 ggttcgtcat gcatctacc gaagtacgct ccgcaacctt tccacgagag tgctttattg 3240
 actggccctt tggagccac caacgacgcg tatgcatcg ccaagatcgc cggatcctg 3300
 caagttcagg cggtaggag ccaatatggg ctggcggtga tctctcgat gccactaac 3360
 ctctacggac ccggcgacaa cttctccccg tccgggtcgc atctcttgc ggcgctcctc 3420
 cgtcgatatg aggaagccaa agctggtggt gcagaagagg tgacgaattg ggggaccggt 3480
 actccgccc gcgaacttct gcatgtcgac gatctggcga gcgcatgcct gtccctttt 3540
 gaacatttcg atggtccgaa ccacgtcaac gtgggcaccg gcgtcgatca cagcattagc 3600
 gagatcgag acatggctgc tacagcgggt ggctacatcg gcgaaacacg ttgggatcca 3660
 actaaacccg atggaacccc gcgcaacta ttggacgtct ccgcgctacg cgagttgggt 3720
 tggcgcccgc gaatcgact gaaagacggc atcgatgcaa cgggtgctgtg gtaccgcaca 3780
 aatgccgatg ccgtgaggag gtaaagctgc gggtcggccg atgttatccc tccggccgga 3840
 cgggtggggc gacctgccgt cgagtgtac ggcagtcgcc tggccggcga ggcgctggc 3900
 ctatgggagt atccaatagc ctggcttggc tcgcccctac gcattatcag ttgaccgctt 3960
 tcgcgccagc tcgcaggctt gcggcagcat ccggttcagg tctcctcatg gtccggtgtg 4020
 gcacgaccac gcaagctcga accgactcgt ttcccaattt cgcgtgctaa tatcgctcga 4080
 tggatttttt gcgcaacgcc ggcttgatgg ctctgaactg tagtaccgag atgtgcgcc 4140
 acttcgaacg aaagcgccta ttagtaaacc aattcaaagc atacggagtc aacgttgta 4200
 ttgatgtcgg tgctaactcc ggccagttcg gtagcgcttt gcgtcgtgca ggattcaaga 4260
 gccgtatcgt ttcctttgaa cctctttcgg ggccatttgc gcaactaacg cgcaagtcgg 4320
 catcgatcc actatgggag tgtcaccagt atgccctagg cgacgccgat gagacgatta 4380
 ccatcaatgt ggcaggcaat gcgggggcaa gtagttccgt gctgccgatg cttaaaagtc 4440

atcaagatgc ctttcctccc gcgaattata ttggcaccga agacgttgca atacaccgcc 4500
 ttgattcggg tgcacagaa tttctgaacc ctaccgatgt tactttcctg aagatcgacg 4560
 tacagggttt cgagaagcag gttatcacgg gcagtaagtc aacgcttaac gaaagctgcg 4620
 tcggcatgca actcgaactt tcttttatcc cgttgtagca aggtgacatg ctgattcatg 4680
 aagcgcttga acttgcttat tccctaggtt tcagactgac gggtttggtg cccggcttta 4740
 cggatccgcg caatggtcga atgcttcaag ctgacggcat tttcttccgt ggggacgatt 4800
 gacataaatg ctccgtcggc acctgcccg tatccaaacg ggcatctgg tgagccggcc 4860
 tcccgggcac ctaatcgact atctaaattg aggcggccgc gacgtgcggc acgaacaggt 4920
 ggccggctgc tagcggtaca cacgcatga ctgcgccagt gttctcgata attatcccta 4980
 cttcaatgc agcggtagc ctgcaagcct gcctcggaag catcgtaggg cagacctacc 5040
 gggaagtgga agtggtcctt gtcgacggcg gttcgaccga tcggaccctc gacatcgca 5100
 acagtttccg cccggaactc ggctcgcgac tggctggtca cagcgggcc gatgatggc 5160
 cctacgacgc catgaaccgc ggctcgggcg tggccacagg cgaatgggta ctttttttag 5220
 gcgccgacga caccctctac gaaccaacca cgttggccca ggtagccgt tttctcgcg 5280
 accatgcggc aagccatctt gtctatggcg atgttgtgat gcgttcgacg aaaagccggc 5340
 atgccggacc tttcgacctc gaccgctcc tatttgagac gaatttgtgc caccaatcga 5400
 tcttttaccg ccgtgagctt ttcgacggca tcggccctta caacctgcg taccgagct 5460
 gggcggactg ggacttcaat attcgctgct tctccaacc ggcgctgatt acccgctaca 5520
 tggacgtcgt gatctccga tacaacgaca tgaccggctt cagcatgagg caggggactg 5580
 ataaagagtt cagaaaacgg ctgccaatgt acttctgggt tgcagggtg gagacttgca 5640
 ggcgcatgct ggctgttttg aaagacaagg agaatcgccg tctggccttg cgtacgggt 5700
 tgataagggt taaggccgtc tccaaagaac gaagcgcaga accgtagtcg cggatccaca 5760
 ttggacttct ttaacgcgtt tgcgtctga tccaccttc aagccggtc cgcgtaacgc 5820
 ggcgcgaga gagtggctgc atatcgcatc actgttctcg tgccagtgt tggaaagcgt 5880
 cgagcactct ggttcgcgtt cttgacgttc gcgccgctc ctgaggtag cgtgtcacgt 5940
 gactgaagcc aatgagtga actcggcgtc gcgaaaggt tcagtcgcg ttgagcaaga 6000
 caccgcaaga ctactggagt gcgtgcaca gcgcctccag ctgcggctg aaagcggatg 6060
 caaagggatt cgaagcttga gcaacatgcg aaggggagaa cggcctatga ggctgggaca 6120
 ggttttcgat ccgcgcgca atgcaactgc aatggccaag tagaagtccc cgctggtggc 6180
 cagcagaagt cccactccg ctgcgggtg ttggctaatt cttggcggt cccttctgt 6240
 ggtcggcgtg gcgcacccg taggactcgc cggaggtgac gacgatgct gcgtggtgca 6300

gcagccgatac gaggatgctg gcggcggttg tgtgctcggg caggaatcgc cccattgtt 6360
cgaagggcca atgcgaggcg atggccaggg agcggcgctc gtagccggca gccacgagcc 6420
ggaacaacag ttgagtcctg gtgtcgtcga gcggggcgaa gccgatctcg tccaagatga 6480
ccagatccgc gcggagcagg gtgtcgatga tcttgccgac ggtgttgctg gccaggccgc 6540
ggtagaggac ctcgatcagg tcggcgggcg tgaagtagcg gactttgaat ccggcggtga 6600
cggcagcgtg cccgcagccg atgagcaggg gacttttgcc cgtaccaggg ggccaatga 6660
ccgccagggt ctgttggtgc cgaatccatt ccaggctcga caggtagtcg aacgtggctg 6720
cgggtgatcga cgatccggtg acgtcgaacc cgtcgagggt cttggtgacc gggaaggctg 6780
cggccttgag acggttggtg gtgttgagg catcgcgggc agcgatctcg gcctcaacca 6840
acgtccgcag gatctcctcc ggtgtccagc gttgctctt ggcgacttgc aacacctcgg 6900
cggcggtgag gcgcaccgtg gccagcttca accgccgcag cgccgcgtca aggtcagcag 6960
ccagcgggtg cgccgaggac ggtgccaccg gcttggcagc ggtggtcatg aggcggtccc 7020
gtcgggtggtg ttgatcttgt aggcctccaa cgagcgggtc tcgacggtg gcagatcgag 7080
cacgagtgcg tcgccggcgg ggcggggttg tgggtgccc gcgccggcg ccaggatcga 7140
gcgcacgtcg gcagcgcgga accggcgaaa cgcaaccgcc cggcgcagcg cgtcaatcaa 7200
agcctgttcg ccgtggggcg cgccaaggcc gagcagaatg tcgagttcgg atttcagtcg 7260
ggtgttgccg atcgagcag caccgacgag gaactgctgc gcttcgggtc ccaatgcgca 7320
gaatcgttcc tctgcttggg ttttcggggc aggaccacgc gagggtgctg gtctgggtcc 7380
gtcgtagtgt tcacgagga tggacacctc acctgggctg acgagctcgt gctcgccac 7440
gatcacaccg gtgcgaggt ccaacaggat caggcgcca tgatcgacca ccaccgccac 7500
ggtggcaccg acgagccgct gaggcaccga gtaacgagct gagccgtaac ggatgcacga 7560
gaggccgtcg accttacggc gcaccgacc cgagccgatc gtcggccgca gcgagggcag 7620
ctccctcaag acggtgcgct cgtcaaccaa gcgatcgtg ggcacggcg agatctccga 7680
gtggaccgtg gcattgacct cggcgacca tagttgcgcc tggcggtga gggcacgtag 7740
gtcgacctgc tcaccggcta acgcagctc ggtcagcagc ggcaccgcaa ggtcgtcctg 7800
agcgtagcca cagaggttct ccacgatgcc cttcgattgc ggatccgcac cgtggcagaa 7860
gtccggaacg aagccatagt gggacgcgaa tcgcacataa tccggtgttg gaacaacaac 7920
attggcgacg acaccacctt tgaggcagcc catccggtcg gccaggatct tggccggaac 7980
ccaccgatac gcctc 7995

<211> 4435
 <212> DNA
 <213> Mycobacterium

<400> 4

```

ttctactgcc tgacctgagc agcgccgagg cgcgccagcgc gatcactgcg acctgaatgg 60
ccagggtggaa agcgccaccg atccccggcac cgagtgcctg acgattcggga tcccttgcac 120
cacaaccgaga gtgagaccgc catgatgacg aaatatcggc tgggcggagt caacgccgga 180
gtgacaaaag tgagaacccg gtgaagcgag cgcttataac agggatcacg gggcaggatg 240
gttcctacct cgccgagcta ctactgagca agggatacga ggttcacggg ctctgttcgtc 300
gagcttctgac gtttaacacg tcgcgggatcg atcacctcta cgttgaccca caccaaccgg 360
gcgcgcgcctt gttcttgac tatgcagacc tctactgacgg caccgcggtg gtgaccctgc 420
tcagcagtat cgaccggat gaggtctaca acctcgcagc gcagtcctcat gtgcgcgtca 480
gctttgacga gccagtgcac accggagaca ccaccggcat gggatcgatc cgacttctgg 540
aagcagtcgg cctttctcgg gtggactgcc ggttctatca ggcttcctcg tcggagatgt 600
tcggcgcatc tccgccaccg cagaacgaat cgacgcgctt ctatccccgt tcgccatacg 660
gcgcggccaa ggtcttctcg tactggacga ctgcgaacta tcgagaggcg tacggattat 720
tcgcagtga tggcatcttg ttcaaccatg agtccccccg gcgcggcgag actttcgtga 780
cccgaaagat cagcggtgcc gtggcgcgca tccgagctgg ctgccaatcg gaggtctata 840
tgggcaacct cgatgcgatc cgcgactggg gctacgcgcc cgaatatgtc gaggggatgt 900
ggaggatgtt gcaagcgctt gaacctgatg actacgtcct ggcgacaggg cgtggttaca 960
ccgtacgtga gttcgctcaa gctgcttttg accacgtcgg gctcgactgg caaaagcacg 1020
tcaagtittga cgaccgctat ttgcgcccc cagaggctga ttcgctagta ggagatgccg 1080
acagggcggc ccagtcactc ggctggaaaag cttcgggttca tactggtgaa ctgcgcgcga 1140
tcatggtgga cgcgacatc gccgcgtcgg agtgcgatgg cacaccatgg atcgacacgc 1200
cgatggtgcc tggttggggc ggagtaagtt gacgactaca cctgggcctc tggaccgcgc 1260
aacgcccgtg tatatcgccg gtcatcgggg gctggtcggc tcagcgctcg tacgtagatt 1320
tgaggccgag gggttcacca atctcattgt gcgatcacgc gatgagattg atctgacgga 1380
ccgagccgca acgtttgatt ttgtgtctga gacaagacca caggtgatca tcgatgcggc 1440
cgcacgggtc ggcggcacatc tggcgaataa cacctatccc gcggacttct tgtccgaaaa 1500
cctccgaatc cagaccaatt tgctcgacgc agctgtcgcc gtgcgtgtgc cgcggtcctt 1560
tttcctcggg tcgtcatgca tctaccgaa gtacgctccg caacctatcc acgagagtgc 1620
tttattgact ggccctttgg agcccaccaa cgacgcgtat gcgatcgcca agatcgccgg 1680

```

tatcctgcaa gttcaggcgg .ttaggcgcca atatgggctg gcgtggatct ctgcgatgcc 1740
 gactaacctc tacggacccg gcgacaactt ctccccgtcc gggtcgcac tcttgccggc 1800
 gctcatccgt cgatatgagg aagccaaagc tgggtggtgca gaagaggtga cgaattgggg 1860
 gaccggtact ccgcggcgcg aacttctgca tgtcgacgat ctggcgagcg catgcctgtt 1920
 ccttttgaa catttcgatg gtccgaacca cgtcaacgtg ggcaccggcg tcgatcacag 1980
 cattagcgag atcgagaca tggtcgctac ggcggtgggc tacatcgcg aaacacgttg 2040
 ggatccaact aaaccgatg gaaccccgcg caaactattg gacgtctccg cgctacgca 2100
 gttgggttg cgcccgcaa tcgcactgaa agacggcatc gatgcaacgg tgtcgtggtg 2160
 ccgcacaaat gccgatgccc tgaggaggta aagctgcggg ccggccgatg ttatccctcc 2220
 ggcgggacgg gtagggcgac ctgccatcga gtggtacggc agtcgcctgg ccggcgaggg 2280
 gcatggccta tgggagtatc ccatagcctg gcttggtctg cccctacgca ttatcagttg 2340
 accgctttcg cgccagctcg caggctcgcg gcagcatccc gttcaggtct cctcatggtc 2400
 cgggtgtgga cgaccacgca agctcgaacc gactcgtttc ccaatttcgc atgctaatat 2460
 cgctcgatgg attttttgcg caacgcggc ttgatggctc gtaacgttag caccgagatg 2520
 ctgcgccact tcgaacgaaa gcgcctatta gtaaaccaat tcaaagcata cggagtcaac 2580
 gttgttattg atgtcgggtc taactccggc cagttcggta gcgctttcg tcgtgcagga 2640
 ttcaagagcc gtatcgtttc ctttgaacct ctttcggggc catttgcgca actaacggcg 2700
 gagtgcgcat cggatccact atgggagtgt caccagtatg ccttaggcga cgccgatgag 2760
 acgattacca tcaatgtggc aggcaatgcg ggggcaagta gttccgtgct gccgatgctt 2820
 aaaagtcac aagatgcctt tcctcccgcg aattatattg gcaccgaaga cgttgcaata 2880
 caccgccttg attcggttg atcagaatct ctgaacccta ccgatgttac tttcctgaag 2940
 atcgacgtac agggtttcga gaagcaggtt atcgcgggca gtaagtcaac gcttaacgaa 3000
 agctgcgtcg gcatgcaact cgaactttct tttattccgt tgtacgaagg tgacatgctg 3060
 attcatgaag cgcttgaact tgtctattcc ctaggtttca gactgacggg tttgttgccc 3120
 ggatttacgg atccgcgcaa tggtcgaatg cttcaagctg acggcatttt cttccgtggg 3180
 gacgattgac ataaatgctt gcgtcggcac cctgccggta tccaaacggg cgatctggtg 3240
 agccggcctc ccgggcacct aatcgactat ctaaattgag gcggccgcga cgtgcggcac 3300
 gaacaggtgg ccggctgcta gcgttacaca cgatcatgact gcgccagtgt tctcgataat 3360
 tatccctacc ttcaatgcag cggtagcgt gcaagcctgc ctcggaagca tcgtcgggca 3420
 gacctaccgg gaagtggaa tggtccttgt cgacggcggg tcgaccgatc ggacctcga 3480
 catcggaac agtttccgcc cggaactcgg ctccgcactg gtcgttcaca gggggccga 3540

tgatggcccc tacgacgcca tgaaccgcgg cgctggcgta gccacaggcg aatgggtact 3600
 ttttttaggc gccgacgaca cctctacga accaaccacg ttggcccagg tagccgcttt 3660
 tctcggcgac catgcggcaa gccatcttgt ctatggcgat gttgtgatgc gttcgacgaa 3720
 aagccggcat gccggacctt tcgacctcga ccgcctccta tttgagacga atttgtgcc 3780
 ccaatcgatc ttttaccgcc gtgagctttt cgacggcatc ggcccttaca acctgcgcta 3840
 ccgagtctgg gcggactggg acttcaatat tcgctgcttc tccaaccgg cgctgattac 3900
 ccgctacatg gacgtcgtga tttccgaata caacgacatg accggcttca gcatgaggca 3960
 ggggactgat aaagagttca gaaaacggct gccaatgtac ttctgggttg caggggtggga 4020
 gacttgacgg cgcatgctgg cgtttttgaa agacaaggag aatcgccgtc tggccttgcg 4080
 tacgcggttg ataagggtta aggccgtctc caaagaacga agcgcagaac cgtagtcgcg 4140
 gatccacatt ggacttcttt aacgcgtttg cgtcctgac cacttttcaa ccccgttccg 4200
 cgtgacgcgg cgcgacgaga gtggtcgcat atcgcgtcac tgttctcgtg ccagtgcctg 4260
 gaaagcgtcg agcactctgg ttgcggttct tgacgttcgc gcccgcccct agaggtagcg 4320
 tgtcacgtga ctgaagccaa tgagtccaac tcggcgtcgc gaaaggtttc agtcgcggtt 4380
 gagcaagaca ccgcaagact actggagtgc gtgcacaagc gcctccagct caccg 4435

<210> 5
 <211> 378
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(375)

<400> 5
 atg atc gct gtg atc tgg tcg gcg gtg ccg aca gga acc gtc gac ttg 48
 Met Ile Ala Val Ile Trp Ser Ala Val Pro Thr Gly Thr Val Asp Leu
 1 5 10 15
 tcg acg atc acc ttg tac cgg tcg atg tat gac cca atg tcg tcc gca 96
 Ser Thr Ile Thr Leu Tyr Arg Ser Met Tyr Asp Pro Met Ser Ser Ala
 20 25 30
 acc gag aag acg tac gtc agg tcc gcc gcc ccg ctt tca ccc atg ggc 144
 Thr Glu Lys Thr Tyr Val Arg Ser Ala Ala Pro Leu Ser Pro Met Gly
 35 40 45
 gtc ggg acg gcg atg aaa atg acg tcc gcg tgc tcg att ccg cgt tgc 192
 Val Gly Thr Ala Met Lys Met Thr Ser Ala Cys Ser Ile Pro Arg Cys
 50 55 60
 cgg tcg gtg gtg aag tca atc agc ccg ttc tca cgg ttc ctc gca atc 240
 Arg Ser Val Val Lys Ser Ile Ser Pro Phe Ser Arg Phe Leu Ala Ile
 65 70 75 80

aac tcc caa ccc ggg ctc gaa aat cgg gac act gcc tgc gag gag caa 288
Asn Ser Gln Pro Gly Leu Glu Asn Arg Asp Thr Ala Cys Glu Glu Gln
85 90 95

atc gat ctt ggc ctg atc gat atc gac aca gac gac atc gtt gcc gct 336
Ile Asp Leu Gly Leu Ile Asp Ile Asp Thr Asp Asp Ile Val Ala Ala
100 105 110

atc cgc gag aca ggc gcc cgt gac gag gcc tac ata gcc tga 378
Ile Arg Glu Thr Gly Ala Arg Asp Glu Ala Tyr Ile Ala
115 120 125

```
<210> 6
<211> 125
<212> PRT
<213> Mycobacterium
```

<400> 6
Met Ile Ala Val Ile Trp Ser Ala Val Pro Thr Gly Thr Val Asp Leu
1 5 10 15

Ser Thr Ile Thr Leu Tyr Arg Ser Met Tyr Asp Pro Met Ser Ser Ala
20 25 30

Thr Glu Lys Thr Tyr Val Arg Ser Ala Ala Pro Leu Ser Pro Met Gly
35 40 45

Val Gly Thr Ala Met Lys Met Thr Ser Ala Cys Ser Ile Pro Arg Cys
50 55 60

Arg Ser Val Val Lys Ser Ile Ser Pro Phe Ser Arg Phe Leu Ala Ile
65 70 75 80

Asn Ser Gln Pro Gly Leu Glu Asn Arg Asp Thr Ala Cys Glu Glu Gln
85 90 95

Ile Asp Leu Gly Leu Ile Asp Ile Asp Thr Asp Asp Ile Val Ala Ala
100 105 110

Ile Arg Glu Thr Gly Ala Arg Asp Glu Ala Tyr Ile Ala
115 120 125

```
<210> 7
<211> 834
<212> DNA
<213> Mycobacterium
```

```
<220>  
<221> CDS  
<222> (1)..(831)
```

<400> 7
gtg tca tct gct cca acc gtg tcg gtg ata acg att tcg ctg aac gat 48
Val Ser Ser Ala Pro Thr Val Ser Val Ile Thr Ile Ser Leu Asn Asp
1 5 10 15

ctc gag gga ttg aaa agc acc gtg gag agc gtt cgc gcg cag cgc tat	96
Leu Glu Gly Leu Lys Ser Thr Val Glu Ser Val Arg Ala Gln Arg Tyr	
20 25 30	
ggg ggg cga atc gag cac atc gtc atc gac ggt gga tcg ggc gac gcc	144
Gly Gly Arg Ile Glu His Ile Val Ile Asp Gly Gly Ser Gly Asp Ala	
35 40 45	
gtc gtg gag tat ctg tcc ggc gat cct ggc ttt gca tat tgg caa tct	192
Val Val Glu Tyr Leu Ser Gly Asp Pro Gly Phe Ala Tyr Trp Gln Ser	
50 55 60	
cag ccc gac aac ggg aga tat gac gcg atg aat cag ggc att gcc cat	240
Gln Pro Asp Asn Gly Arg Tyr Asp Ala Met Asn Gln Gly Ile Ala His	
65 70 75 80	
tcg tcg ggc gac ctg ttg tgg ttt atg cac tcc acg gat cgt ttc tcc	288
Ser Ser Gly Asp Leu Leu Trp Phe Met His Ser Thr Asp Arg Phe Ser	
85 90 95	
gat cca gat gca gtc gct tcc gtg gtg gag gcg ctc tcg ggg cat gga	336
Asp Pro Asp Ala Val Ala Ser Val Val Glu Ala Leu Ser Gly His Gly	
100 105 110	
cca gta cgt gat ttg tgg ggt tac ggg aaa aac aac ctt gtc gga ctc	384
Pro Val Arg Asp Leu Trp Gly Tyr Gly Lys Asn Asn Leu Val Gly Leu	
115 120 125	
gac ggc aaa cca ctt ttc cct cgg ccg tac ggc tat atg ccg ttt aag	432
Asp Gly Lys Pro Leu Phe Pro Arg Pro Tyr Gly Tyr Met Pro Phe Lys	
130 135 140	
atg cgg aaa ttt ctg ctc ggc gcg acg gtt gcg cat cag gcg aca ttc	480
Met Arg Lys Phe Leu Leu Gly Ala Thr Val Ala His Gln Ala Thr Phe	
145 150 155 160	
ttc ggc gcg tcg ctg gta gcc aag ttg ggc ggt tac gat ctt gat ttt	528
Phe Gly Ala Ser Leu Val Ala Lys Leu Gly Gly Tyr Asp Leu Asp Phe	
165 170 175	
gga ctc gag gcg gac cag ctg ttc atc tac cgt gcc gca cta ata ccg	576
Gly Leu Glu Ala Asp Gln Leu Phe Ile Tyr Arg Ala Ala Leu Ile Arg	
180 185 190	
cct ccc gtc acg atc gac cgc gtg gtt tgc gac ttc gat gtc acg gga	624
Pro Pro Val Thr Ile Asp Arg Val Val Cys Asp Phe Asp Val Thr Gly	
195 200 205	
cct ggt tca acc cag ccc atc cgt gag cac tat cgg acc ctg cgg cgg	672
Pro Gly Ser Thr Gln Pro Ile Arg Glu His Tyr Arg Thr Leu Arg Arg	
210 215 220	
ctc tgg gac ctg cat ggc gac tac ccg ctg ggt ggg cgc aga gtg tcg	720
Leu Trp Asp Leu His Gly Asp Tyr Pro Leu Gly Gly Arg Arg Val Ser	
225 230 235 240	
tgg gct tac ttg cgt gtg aag gag tac ttg att cgg gcc gac ctg gcc	768
Trp Ala Tyr Leu Arg Val Lys Glu Tyr Leu Ile Arg Ala Asp Leu Ala	
245 250 255	

gca ttc aac gcg gta aag ttc ttg cga gcg aag ttc gcc aga gct tcg 816
 Ala Phe Asn Ala Val Lys Phe Leu Arg Ala Lys Phe Ala Arg Ala Ser
 260 265 270

cgg aag caa aat tca tag 834
 Arg Lys Gln Asn Ser
 275

<210> 8
 <211> 277
 <212> PRT
 <213> Mycobacterium

<400> 8
 Val Ser Ser Ala Pro Thr Val Ser Val Ile Thr Ile Ser Leu Asn Asp
 1 5 10 15
 Leu Glu Gly Leu Lys Ser Thr Val Glu Ser Val Arg Ala Gln Arg Tyr
 20 25 30
 Gly Gly Arg Ile Glu His Ile Val Ile Asp Gly Gly Ser Gly Asp Ala
 35 40 45
 Val Val Glu Tyr Leu Ser Gly Asp Pro Gly Phe Ala Tyr Trp Gln Ser
 50 55 60
 Gln Pro Asp Asn Gly Arg Tyr Asp Ala Met Asn Gln Gly Ile Ala His
 65 70 75 80
 Ser Ser Gly Asp Leu Leu Trp Phe Met His Ser Thr Asp Arg Phe Ser
 85 90 95
 Asp Pro Asp Ala Val Ala Ser Val Val Glu Ala Leu Ser Gly His Gly
 100 105 110
 Pro Val Arg Asp Leu Trp Gly Tyr Gly Lys Asn Asn Leu Val Gly Leu
 115 120 125
 Asp Gly Lys Pro Leu Phe Pro Arg Pro Tyr Gly Tyr Met Pro Phe Lys
 130 135 140
 Met Arg Lys Phe Leu Leu Gly Ala Thr Val Ala His Gln Ala Thr Phe
 145 150 155 160
 Phe Gly Ala Ser Leu Val Ala Lys Leu Gly Gly Tyr Asp Leu Asp Phe
 165 170 175
 Gly Leu Glu Ala Asp Gln Leu Phe Ile Tyr Arg Ala Ala Leu Ile Arg
 180 185 190
 Pro Pro Val Thr Ile Asp Arg Val Val Cys Asp Phe Asp Val Thr Gly
 195 200 205
 Pro Gly Ser Thr Gln Pro Ile Arg Glu His Tyr Arg Thr Leu Arg Arg
 210 215 220
 Leu Trp Asp Leu His Gly Asp Tyr Pro Leu Gly Gly Arg Arg Val Ser
 225 230 235 240

Trp Ala Tyr Leu Arg Val Lys Glu Tyr Leu Ile Arg Ala Asp Leu Ala
 245 250 255

Ala Phe Asn Ala Val Lys Phe Leu Arg Ala Lys Phe Ala Arg Ala Ser
 260 265 270

Arg Lys Gln Asn Ser
 275

<210> 9
 <211> 1032
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(1029)

<400> 9
 gtg aag cga gcg ctt ata aca ggg atc acg ggg cag gat ggt tcc tac 48
 Val Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr
 1 5 10 15
 ctc gcc gag cta cta ctg agc aag gga tac gag gtt cac ggg ctc gtt 96
 Leu Ala Glu Leu Leu Leu Ser Lys Gly Tyr Glu Val His Gly Leu Val
 20 25 30
 cgt cga gct tcg acg ttt aac acg tcg cgg atc gat cac ctc tac gtt 144
 Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val
 35 40 45
 gac cca cac caa ccg ggc gcg cgc ttg ttc ttg cac tat gca gac ctc 192
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Ala Asp Leu
 50 55 60
 act gac ggc acc cgg ttg gtg acc ctg ctc agc agt atc gac ccg gat 240
 Thr Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Ser Ile Asp Pro Asp
 65 70 75 80
 gag gtc tac aac ctc gca gcg cag tcc cat gtg cgc gtc agc ttt gac 288
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp
 85 90 95
 gag cca gtg cat acc gga gac acc acc ggc atg gga tcg atc cga ctt 336
 Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Ile Arg Leu
 100 105 110
 ctg gaa gca gtc cgc ctt tct cgg gtg gac tgc cgg ttc tat cag gct 384
 Leu Glu Ala Val Arg Leu Ser Arg Val Asp Cys Arg Phe Tyr Gln Ala
 115 120 125
 tcc tcg tcg gag atg ttc ggc gca tct ccg cca ccg cag aac gaa tcg 432
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Ser
 130 135 140
 acg ccg ttc tat ccc cgt tcg cca tac ggc gcg gcc aag gtc ttc tcg 480
 Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Phe Ser
 145 150 155 160

tac tgg acg act cgc aac tat cga gag gcg tac gga tta ttc gca gtg	528
Tyr Trp Thr Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val	
165 170 175	
aat ggc atc ttg ttc aac cat gag tcc ccc cgg cgc ggc gag act ttc	576
Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe	
180 185 190	
gtg acc cga aag atc acg cgt gcc gtg gcg cgc atc cga gct ggc gtc	624
Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Arg Ala Gly Val	
195 200 205	
caa tcg gag gtc tat atg ggc aac ctc gat gcg atc cgc gac tgg ggc	672
Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Ile Arg Asp Trp Gly	
210 215 220	
tac gcg ccc gaa tat gtc gag ggg atg tgg agg atg ttg caa gcg cct	720
Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Ala Pro	
225 230 235 240	
gaa cct gat gac tac gtc ctg gcg aca ggg cgt ggt tac acc gta cgt	768
Glu Pro Asp Asp Tyr Val Leu Ala Thr Gly Arg Gly Tyr Thr Val Arg	
245 250 255	
gag ttc gct caa gct gct ttt gac cat gtc ggg ctc gac tgg caa aag	816
Glu Phe Ala Gln Ala Ala Phe Asp His Val Gly Leu Asp Trp Gln Lys	
260 265 270	
cgc gtc aag ttt gac gac cgc tat ttg cgt ccc acc gag gtc gat tcg	864
Arg Val Lys Phe Asp Asp Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser	
275 280 285	
cta gta gga gat gcc gac aag gcg gcc cag tca ctc ggc tgg aaa gct	912
Leu Val Gly Asp Ala Asp Lys Ala Ala Gln Ser Leu Gly Trp Lys Ala	
290 295 300	
tcg gtt cat act ggt gaa ctc gcg cgc atc atg gtg gac gcg gac atc	960
Ser Val His Thr Gly Glu Leu Ala Arg Ile Met Val Asp Ala Asp Ile	
305 310 315 320	
gcc gcg ttg gag tgc gat gcc aca cca tgg atc gac acg ccg atg ttg	1008
Ala Ala Leu Glu Cys Asp Gly Thr Pro Trp Ile Asp Thr Pro Met Leu	
325 330 335	
cct ggt tgg ggc aga gta agt tga	1032
Pro Gly Trp Gly Arg Val Ser	
340	

<210> 10

<211> 343

<212> PRT

<213> Mycobacterium

<400> 10

Val Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr
1 5 10 15

Leu Ala Glu Leu Leu Leu Ser Lys Gly Tyr Glu Val His Gly Leu Val
20 25 30

Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val
 35 40 45
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Ala Asp Leu
 50 55 60
 Thr Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Ser Ile Asp Pro Asp
 65 70 75 80
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp
 85 90 95
 Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Ile Arg Leu
 100 105 110
 Leu Glu Ala Val Arg Leu Ser Arg Val Asp Cys Arg Phe Tyr Gln Ala
 115 120 125
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Ser
 130 135 140
 Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Phe Ser
 145 150 155 160
 Tyr Trp Thr Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val
 165 170 175
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe
 180 185 190
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Arg Ala Gly Val
 195 200 205
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Ile Arg Asp Trp Gly
 210 215 220
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Ala Pro
 225 230 235 240
 Glu Pro Asp Asp Tyr Val Leu Ala Thr Gly Arg Gly Tyr Thr Val Arg
 245 250 255
 Glu Phe Ala Gln Ala Ala Phe Asp His Val Gly Leu Asp Trp Gln Lys
 260 265 270
 Arg Val Lys Phe Asp Asp Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser
 275 280 285
 Leu Val Gly Asp Ala Asp Lys Ala Ala Gln Ser Leu Gly Trp Lys Ala
 290 295 300
 Ser Val His Thr Gly Glu Leu Ala Arg Ile Met Val Asp Ala Asp Ile
 305 310 315 320
 Ala Ala Leu Glu Cys Asp Gly Thr Pro Trp Ile Asp Thr Pro Met Leu
 325 330 335
 Pro Gly Trp Gly Arg Val Ser
 340

<210> 11
 <211> 1032
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(1029)

<400> 11
 gtg aag cga gcg ctt ata aca ggg atc acg ggg cag gat ggt tcc tac 48
 Val Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr
 1 5 10 15
 ctc gcc gag cta cta ctg agc aag gga tac gag gtt cac ggg ctc gtt 96
 Leu Ala Glu Leu Leu Ser Lys Gly Tyr Glu Val His Gly Leu Val
 20 25 30
 cgt cga gct tcg acg ttt aac acg tcg cgg atc gat cac ctc tac gtt 144
 Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val
 35 40 45
 gac cca cac caa ccg ggc gcg cgc ttg ttc ttg cac tat gca gac ctc 192
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Ala Asp Leu
 50 55 60
 act gac ggc acc cgg ttg gtg acc ctg ctc agc agt atc gac ccg gat 240
 Thr Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Ser Ile Asp Pro Asp
 65 70 75 80
 gag gtc tac aac ctc gca gcg cag tcc cat gtg cgc gtc agc ttt gac 288
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp
 85 90 95
 gag cca gtg cat acc gga gac acc acc ggc atg gga tcg atc cga ctt 336
 Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Ile Arg Leu
 100 105 110
 ctg gaa gca gtc cgc ctt tct cgg gtg gac tgc cgg ttc tat cag gct 384
 Leu Glu Ala Val Arg Leu Ser Arg Val Asp Cys Arg Phe Tyr Gln Ala
 115 120 125
 tcc tcg tcg gag atg ttc ggc gca tct ccg cca ccg cag aac gaa tcg 432
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Ser
 130 135 140
 acg ccg ttc tat ccc cgt tcg cca tac ggc gcg gcc aag gtc ttc tcg 480
 Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Phe Ser
 145 150 155 160
 tac tgg acg act cgc aac tat cga gag gcg tac gga tta ttc gca gtg 528
 Tyr Trp Thr Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val
 165 170 175
 aat ggc atc ttg ttc aac cat gag tcc ccc cgg cgc ggc gag act ttc 576
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe
 180 185 190
 gtg acc cga aag atc acg cgt gcc gtg gcg cgc atc cga gct ggc gtc 624
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Arg Ala Gly Val
 195 200 205

caa tcg gag gtc tat atg ggc aac ctc gat gcg atc cgc gac tgg ggc 672
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Ile Arg Asp Trp Gly
 210 215 220
 tac gcg ccc gaa tat gtc gag ggg atg tgg agg atg ttg caa gcg cct 720
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Ala Pro
 225 230 235 240
 gaa cct gat gac tac gtc ctg gcg aca ggg cgt ggt tac acc gta cgt 768
 Glu Pro Asp Asp Tyr Val Leu Ala Thr Gly Arg Gly Tyr Thr Val Arg
 245 250 255
 gag ttc gct caa gct gct ttt gac cac gtc ggg ctc gac tgg caa aag 816
 Glu Phe Ala Gln Ala Ala Phe Asp His Val Gly Leu Asp Trp Gln Lys
 260 265 270
 cac gtc aag ttt gac gac cgc tat ttg cgc ccc acc gag gtc gat tcg 864
 His Val Lys Phe Asp Asp Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser
 275 280 285
 cta gta gga gat gcc gac agg gcg gcc cag tca ctc ggc tgg aaa gct 912
 Leu Val Gly Asp Ala Asp Arg Ala Ala Gln Ser Leu Gly Trp Lys Ala
 290 295 300
 tcg gtt cat act ggt gaa ctc gcg cgc atc atg gtg gac gcg gac atc 960
 Ser Val His Thr Gly Glu Leu Ala Arg Ile Met Val Asp Ala Asp Ile
 305 310 315 320
 gcc gcg tcg gag tgc gat ggc aca cca tgg atc gac acg ccg atg ttg 1008
 Ala Ala Ser Glu Cys Asp Gly Thr Pro Trp Ile Asp Thr Pro Met Leu
 325 330 335
 cct ggt tgg ggc gga gta agt tga 1032
 Pro Gly Trp Gly Gly Val Ser
 340

<210> 12
 <211> 343
 <212> PRT
 <213> Mycobacterium

<400> 12
 Val Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr
 1 5 10 15
 Leu Ala Glu Leu Leu Leu Ser Lys Gly Tyr Glu Val His Gly Leu Val
 20 25 30
 Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val
 35 40 45
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Ala Asp Leu
 50 55 60
 Thr Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Ser Ile Asp Pro Asp
 65 70 75 80
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp
 85 90 95

Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Ile Arg Leu
 100 105 110
 Leu Glu Ala Val Arg Leu Ser Arg Val Asp Cys Arg Phe Tyr Gln Ala
 115 120 125
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Ser
 130 135 140
 Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Phe Ser
 145 150 155 160
 Tyr Trp Thr Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val
 165 170 175
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe
 180 185 190
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Arg Ala Gly Val
 195 200 205
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Ile Arg Asp Trp Gly
 210 215 220
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Ala Pro
 225 230 235 240
 Glu Pro Asp Asp Tyr Val Leu Ala Thr Gly Arg Gly Tyr Thr Val Arg
 245 250 255
 Glu Phe Ala Gln Ala Ala Phe Asp His Val Gly Leu Asp Trp Gln Lys
 260 265 270
 His Val Lys Phe Asp Asp Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser
 275 280 285
 Leu Val Gly Asp Ala Asp Arg Ala Ala Gln Ser Leu Gly Trp Lys Ala
 290 295 300
 Ser Val His Thr Gly Glu Leu Ala Arg Ile Met Val Asp Ala Asp Ile
 305 310 315 320
 Ala Ala Ser Glu Cys Asp Gly Thr Pro Trp Ile Asp Thr Pro Met Leu
 325 330 335
 Pro Gly Trp Gly Gly Val Ser
 340

<210> 13
 <211> 1020
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(1017)

<400> 13

gtg cga tgg cac acc atg gat cga cac gcc gat gtt gcc tgg ttg ggg	48
Val Arg Trp His Thr Met Asp Arg His Ala Asp Val Ala Trp Leu Gly	
1 5 10 15	
cag agt aag ttg acg act aca cct ggg cct ctg gac cgc gca acg ccc	96
Gln Ser Lys Leu Thr Thr Thr Pro Gly Pro Leu Asp Arg Ala Thr Pro	
20 25 30	
gtg tat atc gcc ggt cat cgg ggg ctg gtc ggc tca gcg ctc gta cgt	144
Val Tyr Ile Ala Gly His Arg Gly Leu Val Gly Ser Ala Leu Val Arg	
35 40 45	
aga ttt gag gcc gag ggg ttc acc aat ctc att gtg cga tca cgc gat	192
Arg Phe Glu Ala Glu Gly Phe Thr Asn Leu Ile Val Arg Ser Arg Asp	
50 55 60	
gag att gat ctg acg gac cga gcc gca acg ttt gat ttt gtg tct gag	240
Glu Ile Asp Leu Thr Asp Arg Ala Ala Thr Phe Asp Phe Val Ser Glu	
65 70 75 80	
aca aga cca cag gtg atc atc gat gcg gcc gca cgg gtc ggc ggc atc	288
Thr Arg Pro Gln Val Ile Ile Asp Ala Ala Arg Val Gly Gly Ile	
85 90 95	
atg gcg aat aac acc tat ccc gcg gac ttc ttg tcc gaa aac ctc cga	336
Met Ala Asn Asn Thr Tyr Pro Ala Asp Phe Leu Ser Glu Asn Leu Arg	
100 105 110	
atc cag acc aat ttg ctc gac gca gct gtc gcc gtg cgt gtg ccg cgg	384
Ile Gln Thr Asn Leu Leu Asp Ala Ala Val Ala Val Arg Val Pro Arg	
115 120 125	
ctc ctt ttc ctc ggt tcg tca tgc atc tac ccg aag tac gct ccg caa	432
Leu Leu Phe Leu Gly Ser Ser Cys Ile Tyr Pro Lys Tyr Ala Pro Gln	
130 135 140	
cct atc cac gag agt gct tta ttg act ggc cct ttg gag ccc acc aac	480
Pro Ile His Glu Ser Ala Leu Leu Thr Gly Pro Leu Glu Pro Thr Asn	
145 150 155 160	
gac gcg tat gcg atc gcc aag atc gcc ggt atc ctg caa gtt cag gcg	528
Asp Ala Tyr Ala Ile Ala Lys Ile Ala Gly Ile Leu Gln Val Gln Ala	
165 170 175	
gtt agg cgc caa tat ggg ctg gcg tgg atc tct gcg atg ccg act aac	576
Val Arg Arg Gln Tyr Gly Leu Ala Trp Ile Ser Ala Met Pro Thr Asn	
180 185 190	
ctc tac gga ccc ggc gac aac ttc tcc ccg tcc ggg tcg cat ctc ttg	624
Leu Tyr Gly Pro Gly Asp Asn Phe Ser Pro Ser Gly Ser His Leu Leu	
195 200 205	
ccg gcg ctc atc cgt cga tat gag gaa gcc aaa gct ggt ggt gca gaa	672
Pro Ala Leu Ile Arg Arg Tyr Glu Glu Ala Lys Ala Gly Gly Ala Glu	
210 215 220	
gag gtg acg aat tgg ggg acc ggt act ccg cgg cgc gaa ctt ctg cat	720
Glu Val Thr Asn Trp Gly Thr Gly Thr Pro Arg Arg Glu Leu Leu His	
225 230 235 240	

gtc gac gat ctg gcg agc gca tgc ctg ttc ctt ttg gaa cat ttc gat 768
 Val Asp Asp Leu Ala Ser Ala Cys Leu Phe Leu Leu Glu His Phe Asp 255
 245 250

ggt ccg aac cac gtc aac gtg ggc acc ggc gtc gat cac agc att agc 816
 Gly Pro Asn His Val Asn Val Gly Thr Gly Val Asp His Ser Ile Ser 270
 260 265

gag atc gca gac atg gtc gct aca gcg gtg ggc tac atc ggc gaa aca 864
 Glu Ile Ala Asp Met Val Ala Thr Ala Val Gly Tyr Ile Gly Glu Thr 285
 275 280

cgt tgg gat cca act aaa ccc gat gga acc ccg cgc aaa cta ttg gac 912
 Arg Trp Asp Pro Thr Lys Pro Asp Gly Thr Pro Arg Lys Leu Leu Asp 300
 290 295

gtc tcc gcg cta cgc gag ttg ggt tgg cgc ccg cga atc gca ctg aaa 960
 Val Ser Ala Leu Arg Glu Leu Gly Trp Arg Pro Arg Ile Ala Leu Lys 320
 305 310 315

gac ggc atc gat gca acg gtg tgc tgg tac cgc aca aat gcc gat gcc 1008
 Asp Gly Ile Asp Ala Thr Val Ser Trp Tyr Arg Thr Asn Ala Asp Ala 335
 325 330

gtg agg agg taa 1020
 Val Arg Arg

<210> 14
 <211> 339
 <212> PRT
 <213> Mycobacterium

<400> 14
 Val Arg Trp His Thr Met Asp Arg His Ala Asp Val Ala Trp Leu Gly 15
 1 5 10

Gln Ser Lys Leu Thr Thr Thr Pro Gly Pro Leu Asp Arg Ala Thr Pro 30
 20 25

Val Tyr Ile Ala Gly His Arg Gly Leu Val Gly Ser Ala Leu Val Arg 45
 35 40

Arg Phe Glu Ala Glu Gly Phe Thr Asn Leu Ile Val Arg Ser Arg Asp 60
 50 55

Glu Ile Asp Leu Thr Asp Arg Ala Ala Thr Phe Asp Phe Val Ser Glu 80
 65 70 75

Thr Arg Pro Gln Val Ile Ile Asp Ala Ala Ala Arg Val Gly Gly Ile 95
 85 90

Met Ala Asn Asn Thr Tyr Pro Ala Asp Phe Leu Ser Glu Asn Leu Arg 110
 100 105

Ile Gln Thr Asn Leu Leu Asp Ala Ala Val Ala Val Arg Val Pro Arg 125
 115 120

Leu Leu Phe Leu Gly Ser Ser Cys Ile Tyr Pro Lys Tyr Ala Pro Gln 140
 130 135

Pro Ile His Glu Ser Ala Leu Leu Thr Gly Pro Leu Glu Pro Thr Asn
 145 150 155 160
 Asp Ala Tyr Ala Ile Ala Lys Ile Ala Gly Ile Leu Gln Val Gln Ala
 165 170 175
 Val Arg Arg Gln Tyr Gly Leu Ala Trp Ile Ser Ala Met Pro Thr Asn
 180 185 190
 Leu Tyr Gly Pro Gly Asp Asn Phe Ser Pro Ser Gly Ser His Leu Leu
 195 200 205
 Pro Ala Leu Ile Arg Arg Tyr Glu Glu Ala Lys Ala Gly Gly Ala Glu
 210 215 220
 Glu Val Thr Asn Trp Gly Thr Gly Thr Pro Arg Arg Glu Leu Leu His
 225 230 235 240
 Val Asp Asp Leu Ala Ser Ala Cys Leu Phe Leu Leu Glu His Phe Asp
 245 250 255
 Gly Pro Asn His Val Asn Val Gly Thr Gly Val Asp His Ser Ile Ser
 260 265 270
 Glu Ile Ala Asp Met Val Ala Thr Ala Val Gly Tyr Ile Gly Glu Thr
 275 280 285
 Arg Trp Asp Pro Thr Lys Pro Asp Gly Thr Pro Arg Lys Leu Leu Asp
 290 295 300
 Val Ser Ala Leu Arg Glu Leu Gly Trp Arg Pro Arg Ile Ala Leu Lys
 305 310 315 320
 Asp Gly Ile Asp Ala Thr Val Ser Trp Tyr Arg Thr Asn Ala Asp Ala
 325 330 335
 Val Arg Arg

<210> 15
 <211> 1020
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(1017)

<400> 15
 gtg cga tgg cac acc atg gat cga cac gcc gat gtt gcc tgg ttg ggg 48
 Val Arg Trp His Thr Met Asp Arg His Ala Asp Val Ala Trp Leu Gly
 1 5 10 15
 cgg agt aag ttg acg act aca cct ggg cct ctg gac cgc gca acg ccc 96
 Arg Ser Lys Leu Thr Thr Pro Gly Pro Leu Asp Arg Ala Thr Pro
 20 25 30
 gtg tat atc gcc ggt cat cgg ggg ctg gtc ggc tca gcg ctc gta cgt 144
 Val Tyr Ile Ala Gly His Arg Gly Leu Val Gly Ser Ala Leu Val Arg
 35 40 45

aga ttt gag gcc gag ggg ttc acc aat ctc att gtg cga tca cgc gat	192
Arg Phe Glu Ala Glu Gly Phe Thr Asn Leu Ile Val Arg Ser Arg Asp	
50 55 60	
gag att gat ctg acg gac cga gcc gca acg ttt gat ttt gtg tct gag	240
Glu Ile Asp Leu Thr Asp Arg Ala Ala Thr Phe Asp Phe Val Ser Glu	
65 70 75 80	
aca aga cca cag gtg atc atc gat gcg gcc gca cgg gtc ggc ggc atc	288
Thr Arg Pro Gln Val Ile Ile Asp Ala Ala Ala Arg Val Gly Gly Ile	
85 90 95	
atg gcg aat aac acc tat ccc gcg gac ttc ttg tcc gaa aac ctc cga	336
Met Ala Asn Asn Thr Tyr Pro Ala Asp Phe Leu Ser Glu Asn Leu Arg	
100 105 110	
atc cag acc aat ttg ctc gac gca gct gtc gcc gtg cgt gtg ccg cgg	384
Ile Gln Thr Asn Leu Leu Asp Ala Ala Val Ala Val Arg Val Pro Arg	
115 120 125	
ctc ctt ttc ctc ggt tcg tca tgc atc tac ccg aag tac gct ccg caa	432
Leu Leu Phe Leu Gly Ser Ser Cys Ile Tyr Pro Lys Tyr Ala Pro Gln	
130 135 140	
cct atc cac gag agt gct tta ttg act gcc cct ttg gag ccc acc aac	480
Pro Ile His Glu Ser Ala Leu Leu Thr Gly Pro Leu Glu Pro Thr Asn	
145 150 155 160	
gac gcg tat gcg atc gcc aag atc gcc ggt atc ctg caa gtt cag gcg	528
Asp Ala Tyr Ala Ile Ala Lys Ile Ala Gly Ile Leu Gln Val Gln Ala	
165 170 175	
gtt agg cgc caa tat ggg ctg gcg tgg atc tct gcg atg ccg act aac	576
Val Arg Arg Gln Tyr Gly Leu Ala Trp Ile Ser Ala Met Pro Thr Asn	
180 185 190	
ctc tac gga ccc gcc gac aac ttc tcc ccg tcc ggg tcg cat ctc ttg	624
Leu Tyr Gly Pro Gly Asp Asn Phe Ser Pro Ser Gly Ser His Leu Leu	
195 200 205	
ccg gcg ctc atc cgt cga tat gag gaa gcc aaa gct ggt ggt gca gaa	672
Pro Ala Leu Ile Arg Arg Tyr Glu Glu Ala Lys Ala Gly Gly Ala Glu	
210 215 220	
gag gtg acg aat tgg ggg acc ggt act ccg cgg cgc gaa ctt ctg cat	720
Glu Val Thr Asn Trp Gly Thr Gly Thr Pro Arg Arg Glu Leu Leu His	
225 230 235 240	
gtc gac gat ctg gcg agc gca tgc ctg ttc ctt ttg gaa cat ttc gat	768
Val Asp Asp Leu Ala Ser Ala Cys Leu Phe Leu Leu Glu His Phe Asp	
245 250 255	
ggt ccg aac cac gtc aac gtg ggc acc ggc gtc gat cac agc att agc	816
Gly Pro Asn His Val Asn Val Gly Thr Gly Val Asp His Ser Ile Ser	
260 265 270	
gag atc gca gac atg gtc gct acg gcg gtg ggc tac atc ggc gaa aca	864
Glu Ile Ala Asp Met Val Ala Thr Ala Val Gly Tyr Ile Gly Glu Thr	
275 280 285	

cgt tgg gat cca act aaa ccc gat gga acc ccg cgc aaa cta ttg gac 912
 Arg Trp Asp Pro Thr Lys Pro Asp Gly Thr Pro Arg Lys Leu Leu Asp
 290 295 300

gtc tcc gcg cta cgc gag ttg ggt tgg cgc ccg cga atc gca ctg aaa 960
 Val Ser Ala Leu Arg Glu Leu Gly Trp Arg Pro Arg Ile Ala Leu Lys
 305 310 315 320

gac ggc atc gat gca acg gtg tgc tgg tac cgc aca aat gcc gat gcc 1008
 Asp Gly Ile Asp Ala Thr Val Ser Trp Tyr Arg Thr Asn Ala Asp Ala
 325 330 335

gtg agg agg taa 1020
 Val Arg Arg

<210> 16
 <211> 339
 <212> PRT
 <213> Mycobacterium

<400> 16
 Val Arg Trp His Thr Met Asp Arg His Ala Asp Val Ala Trp Leu Gly
 1 5 10 15

Arg Ser Lys Leu Thr Thr Thr Pro Gly Pro Leu Asp Arg Ala Thr Pro
 20 25 30

Val Tyr Ile Ala Gly His Arg Gly Leu Val Gly Ser Ala Leu Val Arg
 35 40 45

Arg Phe Glu Ala Glu Gly Phe Thr Asn Leu Ile Val Arg Ser Arg Asp
 50 55 60

Glu Ile Asp Leu Thr Asp Arg Ala Ala Thr Phe Asp Phe Val Ser Glu
 65 70 75 80

Thr Arg Pro Gln Val Ile Ile Asp Ala Ala Ala Arg Val Gly Gly Ile
 85 90 95

Met Ala Asn Asn Thr Tyr Pro Ala Asp Phe Leu Ser Glu Asn Leu Arg
 100 105 110

Ile Gln Thr Asn Leu Leu Asp Ala Ala Val Ala Val Arg Val Pro Arg
 115 120 125

Leu Leu Phe Leu Gly Ser Ser Cys Ile Tyr Pro Lys Tyr Ala Pro Gln
 130 135 140

Pro Ile His Glu Ser Ala Leu Leu Thr Gly Pro Leu Glu Pro Thr Asn
 145 150 155 160

Asp Ala Tyr Ala Ile Ala Lys Ile Ala Gly Ile Leu Gln Val Gln Ala
 165 170 175

Val Arg Arg Gln Tyr Gly Leu Ala Trp Ile Ser Ala Met Pro Thr Asn
 180 185 190

Leu Tyr Gly Pro Gly Asp Asn Phe Ser Pro Ser Gly Ser His Leu Leu
 195 200 205

Pro Ala Leu Ile Arg Arg Tyr Glu Glu Ala Lys Ala Gly Gly Ala Glu
 210 215 220
 Glu Val Thr Asn Trp Gly Thr Gly Thr Pro Arg Arg Glu Leu Leu His
 225 230 235 240
 Val Asp Asp Leu Ala Ser Ala Cys Leu Phe Leu Leu Glu His Phe Asp
 245 250 255
 Gly Pro Asn His Val Asn Val Gly Thr Gly Val Asp His Ser Ile Ser
 260 265 270
 Glu Ile Ala Asp Met Val Ala Thr Ala Val Gly Tyr Ile Gly Glu Thr
 275 280 285
 Arg Trp Asp Pro Thr Lys Pro Asp Gly Thr Pro Arg Lys Leu Leu Asp
 290 295 300
 Val Ser Ala Leu Arg Glu Leu Gly Trp Arg Pro Arg Ile Ala Leu Lys
 305 310 315 320
 Asp Gly Ile Asp Ala Thr Val Ser Trp Tyr Arg Thr Asn Ala Asp Ala
 325 330 335
 Val Arg Arg

<210> 17
 <211> 723
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(720)

<400> 17
 atg gat ttt ttg cgc aac gcc ggc ttg atg gct cgt aac gtt agt acc 48
 Met Asp Phe Leu Arg Asn Ala Gly Leu Met Ala Arg Asn Val Ser Thr
 1 5 10 15
 gag atg ctg cgc cac ttc gaa cga aag cgc cta tta gta aac caa ttc 96
 Glu Met Leu Arg His Phe Glu Arg Lys Arg Leu Leu Val Asn Gln Phe
 20 25 30
 aaa gca tac gga gtc aac gtt gtt att gat gtc ggt gct aac tcc ggc 144
 Lys Ala Tyr Gly Val Asn Val Val Ile Asp Val Gly Ala Asn Ser Gly
 35 40 45
 cag ttc ggt agc gct ttg cgt cgt gca gga ttc aag agc cgt atc gtt 192
 Gln Phe Gly Ser Ala Leu Arg Arg Ala Gly Phe Lys Ser Arg Ile Val
 50 55 60
 tcc ttt gaa cct ctt tcg ggg cca ttt gcg caa cta acg cgc aag tcg 240
 Ser Phe Glu Pro Leu Ser Gly Pro Phe Ala Gln Leu Thr Arg Lys Ser
 65 70 75 80
 gca tcg gat cca cta tgg gag tgt cac cag tat gcc cta ggc gac gcc 288
 Ala Ser Asp Pro Leu Trp Glu Cys His Gln Tyr Ala Leu Gly Asp Ala
 85 90 95

gat gag acg att acc atc aat gtg gca ggc aat gcg ggg gca agt agt 336
 Asp Glu Thr Ile Thr Ile Asn Val Ala Gly Asn Ala Gly Ala Ser Ser
 100 105 110
 tcc gtg ctg ccg atg ctt aaa agt cat caa gat gcc ttt cct ccc gcg 384
 Ser Val Leu Pro Met Leu Lys Ser His Gln Asp Ala Phe Pro Pro Ala
 115 120 125
 aat tat att ggc acc gaa gac gtt gca ata cac cgc ctt gat tcg gtt 432
 Asn Tyr Ile Gly Thr Glu Asp Val Ala Ile His Arg Leu Asp Ser Val
 130 135 140
 gca tca gaa ttt ctg aac cct acc gat gtt act ttc ctg aag atc gac 480
 Ala Ser Glu Phe Leu Asn Pro Thr Asp Val Thr Phe Leu Lys Ile Asp
 145 150 155 160
 gta cag ggt ttc gag aag cag gtt atc acg ggc agt aag tca acg ctt 528
 Val Gln Gly Phe Glu Lys Gln Val Ile Thr Gly Ser Lys Ser Thr Leu
 165 170 175
 aac gaa agc tgc gtc ggc atg caa ctc gaa ctt tct ttt att ccg ttg 576
 Asn Glu Ser Cys Val Gly Met Gln Leu Glu Leu Ser Phe Ile Pro Leu
 180 185 190
 tac gaa ggt gac atg ctg att cat gaa gcg ctt gaa ctt gtc tat tcc 624
 Tyr Glu Gly Asp Met Leu Ile His Glu Ala Leu Glu Leu Val Tyr Ser
 195 200 205
 cta ggt ttc aga ctg acg ggt ttg ttg ccc ggc ttt acg gat ccg cgc 672
 Leu Gly Phe Arg Leu Thr Gly Leu Leu Pro Gly Phe Thr Asp Pro Arg
 210 215 220
 aat ggt cga atg ctt caa gct gac ggc att ttc ttc cgt ggg gac gat 720
 Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg Gly Asp Asp
 225 230 235 240
 tga 723

<210> 18
 <211> 240
 <212> PRT
 <213> Mycobacterium

<400> 18
 Met Asp Phe Leu Arg Asn Ala Gly Leu Met Ala Arg Asn Val Ser Thr
 1 5 10 15
 Glu Met Leu Arg His Phe Glu Arg Lys Arg Leu Leu Val Asn Gln Phe
 20 25 30
 Lys Ala Tyr Gly Val Asn Val Val Ile Asp Val Gly Ala Asn Ser Gly
 35 40 45
 Gln Phe Gly Ser Ala Leu Arg Arg Ala Gly Phe Lys Ser Arg Ile Val
 50 55 60
 Ser Phe Glu Pro Leu Ser Gly Pro Phe Ala Gln Leu Thr Arg Lys Ser
 65 70 75 80

Ala Ser Asp Pro Leu Trp Glu Cys His Gln Tyr Ala Leu Gly Asp Ala
85 90 95

Asp Glu Thr Ile Thr Ile Asn Val Ala Gly Asn Ala Gly Ala Ser Ser
100 105 110

Ser Val Leu Pro Met Leu Lys Ser His Gln Asp Ala Phe Pro Pro Ala
115 120 125

Asn Tyr Ile Gly Thr Glu Asp Val Ala Ile His Arg Leu Asp Ser Val
130 135 140

Ala Ser Glu Phe Leu Asn Pro Thr Asp Val Thr Phe Leu Lys Ile Asp
145 150 155 160

Val Gln Gly Phe Glu Lys Gln Val Ile Thr Gly Ser Lys Ser Thr Leu
165 170 175

Asn Glu Ser Cys Val Gly Met Gln Leu Glu Leu Ser Phe Ile Pro Leu
180 185 190

Tyr Glu Gly Asp Met Leu Ile His Glu Ala Leu Glu Leu Val Tyr Ser
195 200 205

Leu Gly Phe Arg Leu Thr Gly Leu Leu Pro Gly Phe Thr Asp Pro Arg
210 215 220

Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg Gly Asp Asp
225 230 235 240

<210> 19
<211> 723
<212> DNA
<213> Mycobacterium

<220>
<221> CDS
<222> (1)..(720)

<400> 19
atg gat ttt ttg cgc aac gcc ggc ttg atg gct cgt aac gtt agc acc 48
Met Asp Phe Leu Arg Asn Ala Gly Leu Met Ala Arg Asn Val Ser Thr
1 5 10 15

gag atg ctg cgc cac ttc gaa cga aag cgc cta tta gta aac caa ttc 96
Glu Met Leu Arg His Phe Glu Arg Lys Arg Leu Leu Val Asn Gln Phe
20 25 30

aaa gca tac gga gtc aac gtt gtt att gat gtc ggt gct aac tcc ggc 144
Lys Ala Tyr Gly Val Asn Val Val Ile Asp Val Gly Ala Asn Ser Gly
35 40 45

cag ttc ggt agc gct ttg cgt cgt gca gga ttc aag agc cgt atc gtt 192
Gln Phe Gly Ser Ala Leu Arg Arg Ala Gly Phe Lys Ser Arg Ile Val
50 55 60

tcc ttt gaa cct ctt tcg ggg cca ttt gcg caa cta acg cgc gag tcg 240
Ser Phe Glu Pro Leu Ser Gly Pro Phe Ala Gln Leu Thr Arg Glu Ser
65 70 75 80

gca tgc gat cca cta tgg gag tgt cac cag tat gcc cta ggc gac gcc 288
 Ala Ser Asp Pro Leu Trp Glu Cys His Gln Tyr Ala Leu Gly Asp Ala
 85 90 95

gat gag acg att acc atc aat gtg gca ggc aat gcg ggg gca agt agt 336
 Asp Glu Thr Ile Thr Ile Asn Val Ala Gly Asn Ala Gly Ala Ser Ser
 100 105 110

tcc gtg ctg ccg atg ctt aaa agt cat caa gat gcc ttt cct ccc gcg 384
 Ser Val Leu Pro Met Leu Lys Ser His Gln Asp Ala Phe Pro Pro Ala
 115 120 125

aat tat att ggc acc gaa gac gtt gca ata cac cgc ctt gat tgc gtt 432
 Asn Tyr Ile Gly Thr Glu Asp Val Ala Ile His Arg Leu Asp Ser Val
 130 135 140

gca tca gaa ttt ctg aac cct acc gat gtt act ttc ctg aag atc gac 480
 Ala Ser Glu Phe Leu Asn Pro Thr Asp Val Thr Phe Leu Lys Ile Asp
 145 150 155 160

gta cag ggt ttc gag aag cag gtt atc gcg ggc agt aag tca acg ctt 528
 Val Gln Gly Phe Glu Lys Gln Val Ile Ala Gly Ser Lys Ser Thr Leu
 165 170 175

aac gaa agc tgc gtc ggc atg caa ctc gaa ctt tct ttt att ccg ttg 576
 Asn Glu Ser Cys Val Gly Met Gln Leu Glu Leu Ser Phe Ile Pro Leu
 180 185 190

tac gaa ggt gac atg ctg att cat gaa gcg ctt gaa ctt gtc tat tcc 624
 Tyr Glu Gly Asp Met Leu Ile His Glu Ala Leu Glu Leu Val Tyr Ser
 195 200 205

cta ggt ttc aga ctg acg ggt ttg ttg ccc gga ttt acg gat ccg cgc 672
 Leu Gly Phe Arg Leu Thr Gly Leu Leu Pro Gly Phe Thr Asp Pro Arg
 210 215 220

aat ggt cga atg ctt caa gct gac ggc att ttc ttc cgt ggg gac gat 720
 Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg Gly Asp Asp
 225 230 235 240

tga 723

<210> 20
 <211> 240
 <212> PRT
 <213> Mycobacterium

<400> 20
 Met Asp Phe Leu Arg Asn Ala Gly Leu Met Ala Arg Asn Val Ser Thr
 1 5 10 15

Glu Met Leu Arg His Phe Glu Arg Lys Arg Leu Leu Val Asn Gln Phe
 20 25 30

Lys Ala Tyr Gly Val Asn Val Val Ile Asp Val Gly Ala Asn Ser Gly
 35 40 45

Gln Phe Gly Ser Ala Leu Arg Arg Ala Gly Phe Lys Ser Arg Ile Val
 50 55 60

Ser Phe Glu Pro Leu Ser Gly Pro Phe Ala Gln Leu Thr Arg Glu Ser
 65 70 75 80
 Ala Ser Asp Pro Leu Trp Glu Cys His Gln Tyr Ala Leu Gly Asp Ala
 85 90 95
 Asp Glu Thr Ile Thr Ile Asn Val Ala Gly Asn Ala Gly Ala Ser Ser
 100 105 110
 Ser Val Leu Pro Met Leu Lys Ser His Gln Asp Ala Phe Pro Pro Ala
 115 120 125
 Asn Tyr Ile Gly Thr Glu Asp Val Ala Ile His Arg Leu Asp Ser Val
 130 135 140
 Ala Ser Glu Phe Leu Asn Pro Thr Asp Val Thr Phe Leu Lys Ile Asp
 145 150 155 160
 Val Gln Gly Phe Glu Lys Gln Val Ile Ala Gly Ser Lys Ser Thr Leu
 165 170 175
 Asn Glu Ser Cys Val Gly Met Gln Leu Glu Leu Ser Phe Ile Pro Leu
 180 185 190
 Tyr Glu Gly Asp Met Leu Ile His Glu Ala Leu Glu Leu Val Tyr Ser
 195 200 205
 Leu Gly Phe Arg Leu Thr Gly Leu Leu Pro Gly Phe Thr Asp Pro Arg
 210 215 220
 Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg Gly Asp Asp
 225 230 235 240

<210> 21
 <211> 801
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(798)

<400> 21
 atg act gcg cca gtg ttc tcg ata att atc cct acc ttc aat gca gcg 48
 Met Thr Ala Pro Val Phe Ser Ile Ile Ile Pro Thr Phe Asn Ala Ala
 1 5 10 15
 gtg acg ctg caa gcc tgc ctc gga agc atc gtc ggg cag acc tac cgg 96
 Val Thr Leu Gln Ala Cys Leu Gly Ser Ile Val Gly Gln Thr Tyr Arg
 20 25 30
 gaa gtg gaa gtg gtc ctt gtc gac ggc ggt tcg acc gat cgg acc ctc 144
 Glu Val Glu Val Val Leu Val Asp Gly Gly Ser Thr Asp Arg Thr Leu
 35 40 45
 gac atc gcg aac agt ttc cgc ccg gaa ctc ggc tcg cga ctg gtc gtt 192
 Asp Ile Ala Asn Ser Phe Arg Pro Glu Leu Gly Ser Arg Leu Val Val
 50 55 60

cac agc ggg ccc gat gat ggc cgc tac gac gcc atg aac cgc ggc gtc 240
 His Ser Gly Pro Asp Asp Gly Pro Tyr Asp Ala Met Asn Arg Gly Val
 65 70 75 80

ggc gtg gcc aca ggc gaa tgg gta ctt ttt tta ggc gcc gac gac acc 288
 Gly Val Ala Thr Gly Glu Trp Val Leu Phe Leu Gly Ala Asp Asp Thr
 85 90 95

ctc tac gaa cca acc acg ttg gcc cag gta gcc gct ttt ctc ggc gac 336
 Leu Tyr Glu Pro Thr Thr Leu Ala Gln Val Ala Ala Phe Leu Gly Asp
 100 105 110

cat gcg gca agc cat ctt gtc tat ggc gat gtt gtg atg cgt tcg acg 384
 His Ala Ala Ser His Leu Val Tyr Gly Asp Val Val Met Arg Ser Thr
 115 120 125

aaa agc cgg cat gcc gga cct ttc gac ctc gac cgc ctc cta ttt gag 432
 Lys Ser Arg His Ala Gly Pro Phe Asp Leu Asp Arg Leu Leu Phe Glu
 130 135 140

acg aat ttg tgc cac caa tcg atc ttt tac cgc cgt gag ctt ttc gac 480
 Thr Asn Leu Cys His Gln Ser Ile Phe Tyr Arg Arg Glu Leu Phe Asp
 145 150 155 160

ggc atc ggc cct tac aac ctg cgc tac cga gtc tgg gcg gac tgg gac 528
 Gly Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Trp Ala Asp Trp Asp
 165 170 175

ttc aat att cgc tgc ttc tcc aac ccg gcg ctg att acc cgc tac atg 576
 Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Ile Thr Arg Tyr Met
 180 185 190

gac gtc gtg att tcc gaa tac aac gac atg acc ggc ttc agc atg agg 624
 Asp Val Val Ile Ser Glu Tyr Asn Asp Met Thr Gly Phe Ser Met Arg
 195 200 205

cag ggg act gat aaa gag ttc aga aaa cgg ctg cca atg tac ttc tgg 672
 Gln Gly Thr Asp Lys Glu Phe Arg Lys Arg Leu Pro Met Tyr Phe Trp
 210 215 220

gtt gca ggg tgg gag act tgc agg cgc atg ctg gcg ttt ttg aaa gac 720
 Val Ala Gly Trp Glu Thr Cys Arg Arg Met Leu Ala Phe Leu Lys Asp
 225 230 235 240

aag gag aat cgc cgt ctg gcc ttg cgt acg cgg ttg ata agg gtt aag 768
 Lys Glu Asn Arg Arg Leu Ala Leu Arg Thr Arg Leu Ile Arg Val Lys
 245 250 255

gcc gtc tcc aaa gaa cga agc gca gaa ccg tag 801
 Ala Val Ser Lys Glu Arg Ser Ala Glu Pro
 260 265

<210> 22
 <211> 266
 <212> PRT
 <213> Mycobacterium

<400> 22
 Met Thr Ala Pro Val Phe Ser Ile Ile Ile Pro Thr Phe Asn Ala Ala
 1 5 10 15

Val Thr Leu Gln Ala Cys Leu Gly Ser Ile Val Gly Gln Thr Tyr Arg
 20 25 30
 Glu Val Glu Val Val Leu Val Asp Gly Gly Ser Thr Asp Arg Thr Leu
 35 40 45
 Asp Ile Ala Asn Ser Phe Arg Pro Glu Leu Gly Ser Arg Leu Val Val
 50 55 60
 His Ser Gly Pro Asp Asp Gly Pro Tyr Asp Ala Met Asn Arg Gly Val
 65 70 75 80
 Gly Val Ala Thr Gly Glu Trp Val Leu Phe Leu Gly Ala Asp Asp Thr
 85 90 95
 Leu Tyr Glu Pro Thr Thr Leu Ala Gln Val Ala Ala Phe Leu Gly Asp
 100 105 110
 His Ala Ala Ser His Leu Val Tyr Gly Asp Val Val Met Arg Ser Thr
 115 120 125
 Lys Ser Arg His Ala Gly Pro Phe Asp Leu Asp Arg Leu Leu Phe Glu
 130 135 140
 Thr Asn Leu Cys His Gln Ser Ile Phe Tyr Arg Arg Glu Leu Phe Asp
 145 150 155 160
 Gly Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Trp Ala Asp Trp Asp
 165 170 175
 Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Ile Thr Arg Tyr Met
 180 185 190
 Asp Val Val Ile Ser Glu Tyr Asn Asp Met Thr Gly Phe Ser Met Arg
 195 200 205
 Gln Gly Thr Asp Lys Glu Phe Arg Lys Arg Leu Pro Met Tyr Phe Trp
 210 215 220
 Val Ala Gly Trp Glu Thr Cys Arg Arg Met Leu Ala Phe Leu Lys Asp
 225 230 235 240
 Lys Glu Asn Arg Arg Leu Ala Leu Arg Thr Arg Leu Ile Arg Val Lys
 245 250 255
 Ala Val Ser Lys Glu Arg Ser Ala Glu Pro
 260 265

<210> 23
 <211> 801
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(798)

<400> 23

atg act gcg cca gtg ttc tcg ata att atc cct acc ttc aat gca gcg	48
Met Thr Ala Pro Val Phe Ser Ile Ile Ile Pro Thr Phe Asn Ala Ala	
1 5 10 15	
gtg acg ctg caa gcc tgc ctc gga agc atc gtc ggg cag acc tac cgg	96
Val Thr Leu Gln Ala Cys Leu Gly Ser Ile Val Gly Gln Thr Tyr Arg	
20 25 30	
gaa gtg gaa gtg gtc ctt gtc gac ggc ggt tcg acc gat cgg acc ctc	144
Glu Val Glu Val Val Leu Val Asp Gly Gly Ser Thr Asp Arg Thr Leu	
35 40 45	
gac atc gcg aac agt ttc cgc ccg gaa ctc ggc tcg cga ctg gtc gtt	192
Asp Ile Ala Asn Ser Phe Arg Pro Glu Leu Gly Ser Arg Leu Val Val	
50 55 60	
cac agc ggg ccc gat gat ggc ccc tac gac gcc atg aac cgc ggc gtc	240
His Ser Gly Pro Asp Asp Gly Pro Tyr Asp Ala Met Asn Arg Gly Val	
65 70 75 80	
ggc gta gcc aca ggc gaa tgg gta ctt ttt tta ggc gcc gac gac acc	288
Gly Val Ala Thr Gly Glu Trp Val Leu Phe Leu Gly Ala Asp Asp Thr	
85 90 95	
ctc tac gaa cca acc acg ttg gcc cag gta gcc gct ttt ctc ggc gac	336
Leu Tyr Glu Pro Thr Thr Leu Ala Gln Val Ala Ala Phe Leu Gly Asp	
100 105 110	
cat gcg gca agc cat ctt gtc tat ggc gat gtt gtg atg cgt tcg acg	384
His Ala Ala Ser His Leu Val Tyr Gly Asp Val Val Met Arg Ser Thr	
115 120 125	
aaa agc cgg cat gcc gga cct ttc gac ctc gac cgc ctc cta ttt gag	432
Lys Ser Arg His Ala Gly Pro Phe Asp Leu Asp Arg Leu Leu Phe Glu	
130 135 140	
acg aat ttg tgc cac caa tcg atc ttt tac cgc cgt gag ctt ttc gac	480
Thr Asn Leu Cys His Gln Ser Ile Phe Tyr Arg Arg Glu Leu Phe Asp	
145 150 155 160	
ggc atc ggc cct tac aac ctg cgc tac cga gtc tgg gcg gac tgg gac	528
Gly Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Trp Ala Asp Trp Asp	
165 170 175	
ttc aat att cgc tgc ttc tcc aac ccg gcg ctg att acc cgc tac atg	576
Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Ile Thr Arg Tyr Met	
180 185 190	
gac gtc gtg att tcc gaa tac aac gac atg acc ggc ttc agc atg agg	624
Asp Val Val Ile Ser Glu Tyr Asn Asp Met Thr Gly Phe Ser Met Arg	
195 200 205	
cag ggg act gat aaa gag ttc aga aaa ccg ctg cca atg tac ttc tgg	672
Gln Gly Thr Asp Lys Glu Phe Arg Lys Arg Leu Pro Met Tyr Phe Trp	
210 215 220	
gtt gca ggg tgg gag act tgc agg cgc atg ctg gcg ttt ttg aaa gac	720
Val Ala Gly Trp Glu Thr Cys Arg Arg Met Leu Ala Phe Leu Lys Asp	
225 230 235 240	

801

801

Val	Ala	Gly	Trp	Glu	Thr	Cys	Arg	Arg	Met	Leu	Ala	Phe	Leu	Lys	Asp
225					230					235					240

Lys Glu Asn Arg Arg Leu Ala Leu Arg Thr Arg Leu Ile Arg Val Lys
 245 250 255

Ala Val Ser Lys Glu Arg Ser Ala Glu Pro
 260 265

<210> 25
 <211> 867
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(864)

<400> 25
 gtg gcc agc aga agt ccc cac tcc gct gcg ggt ggt tgg cta att ctt 48
 Val Ala Ser Arg Ser Pro His Ser Ala Ala Gly Gly Trp Leu Ile Leu
 1 5 10 15
 ggc ggc tcc ctt ctt gtg gtc ggc gtg gcg cat ccg gta gga ctc gcc 96
 Gly Gly Ser Leu Leu Val Val Gly Val Ala His Pro Val Gly Leu Ala
 20 25 30
 gga ggt gac gac gat gct ggc gtg gtg cag cag ccg atc gag gat gct 144
 Gly Gly Asp Asp Asp Ala Gly Val Val Gln Gln Pro Ile Glu Asp Ala
 35 40 45
 ggc ggc ggt ggt gtg ctc ggg cag gaa tcg ccc cca ttg ttc gaa ggg 192
 Gly Gly Gly Gly Val Leu Gly Gln Glu Ser Pro Pro Leu Phe Glu Gly
 50 55 60
 cca atg cga ggc gat ggc cag gga gcg gcg ctc gta gcc ggc agc cac 240
 Pro Met Arg Gly Asp Gly Gln Gly Ala Ala Leu Val Ala Gly Ser His
 65 70 75 80
 gag ccg gaa caa cag ttg agt ccc ggt gtc gtc gag ccg ggc gaa gcc 288
 Glu Pro Glu Gln Gln Leu Ser Pro Gly Val Val Glu Arg Gly Glu Ala
 85 90 95
 gat ctc gtc caa gat gac cag atc cgc gcg gag cag ggt gtc gat gat 336
 Asp Leu Val Gln Asp Asp Gln Ile Arg Ala Glu Gln Gly Val Asp Asp
 100 105 110
 ctt gcc gac ggt gtt gtc ggc cag gcc gcg gta gag gac ctc gat cag 384
 Leu Ala Asp Gly Val Val Gly Gln Ala Ala Val Glu Asp Leu Asp Gln
 115 120 125
 gtc ggc ggc ggt gaa gta gcg gac ttt gaa tcc ggc gtg gac ggc agc 432
 Val Gly Gly Gly Glu Val Ala Asp Phe Glu Ser Gly Val Asp Gly Ser
 130 135 140
 gtg ccc gca gcc gat gag cag gtg act ttt gcc cgt acc agg tgg gcc 480
 Val Pro Ala Ala Asp Glu Gln Val Thr Phe Ala Arg Thr Arg Trp Ala
 145 150 155 160
 aat gac cgc cag gtt ctg ttg tgc ccg aat cca ttc cag gct cga cag 528
 Asn Asp Arg Gln Val Leu Leu Cys Pro Asn Pro Phe Gln Ala Arg Gln
 165 170 175

gta gtc gaa cgt ggc tgc ggt gat cga cga tcc ggt gac gtc gaa ccc 576
 Val Val Glu Arg Gly Cys Gly Asp Arg Arg Ser Gly Asp Val Glu Pro
 180 185 190

gtc gag ggt ctt ggt gac cgg gaa ggc tgc ggc ctt gag acg gtt ggc 624
 Val Glu Gly Leu Gly Asp Arg Glu Gly Cys Gly Leu Glu Thr Val Gly
 195 200 205

ggt gtt gga ggc atc gcg ggc agc gat ctc ggc ctc aac caa cgt ccg 672
 Gly Val Gly Gly Ile Ala Gly Ser Asp Leu Gly Leu Asn Gln Arg Pro
 210 215 220

cag gat ctc ctc cgg tgt cca gcg ttg cgt ctt ggc gac ttg caa cac 720
 Gln Asp Leu Leu Arg Cys Pro Ala Leu Arg Leu Gly Asp Leu Gln His
 225 230 235 240

ctc ggc ggc gtt gcg gcg cac cgt ggc cag ctt caa ccg ccg cag cgc 768
 Leu Gly Gly Val Ala Ala His Arg Gly Gln Leu Gln Pro Pro Gln Arg
 245 250 255

cgc gtc aag gtc agc agc cag cgg tgc cgc cga gga cgg tgc cac cgg 816
 Arg Val Lys Val Ser Ser Gln Arg Cys Arg Arg Gly Arg Cys His Arg
 260 265 270

ctt ggc agc ggt ggt cat gag gcc gtc ccg tcg gtg gtg ttg atc ttg 864
 Leu Gly Ser Gly Gly His Glu Ala Val Pro Ser Val Val Leu Ile Leu
 275 280 285

tag 867

<210> 26
 <211> 288
 <212> PRT
 <213> Mycobacterium

<400> 26
 Val Ala Ser Arg Ser Pro His Ser Ala Ala Gly Gly Trp Leu Ile Leu
 1 5 10 15

Gly Gly Ser Leu Leu Val Val Gly Val Ala His Pro Val Gly Leu Ala
 20 25 30

Gly Gly Asp Asp Asp Ala Gly Val Val Gln Gln Pro Ile Glu Asp Ala
 35 40 45

Gly Gly Gly Gly Val Leu Gly Gln Glu Ser Pro Pro Leu Phe Glu Gly
 50 55 60

Pro Met Arg Gly Asp Gly Gln Gly Ala Ala Leu Val Ala Gly Ser His
 65 70 75 80

Glu Pro Glu Gln Gln Leu Ser Pro Gly Val Val Glu Arg Gly Glu Ala
 85 90 95

Asp Leu Val Gln Asp Asp Gln Ile Arg Ala Glu Gln Gly Val Asp Asp
 100 105 110

Leu Ala Asp Gly Val Val Gly Gln Ala Ala Val Glu Asp Leu Asp Gln
 115 120 125

Val Gly Gly Gly Glu Val Ala Asp Phe Glu Ser Gly Val Asp Gly Ser
 130 135 140

Val Pro Ala Ala Asp Glu Gln Val Thr Phe Ala Arg Thr Arg Trp Ala
 145 150 155 160

Asn Asp Arg Gln Val Leu Leu Cys Pro Asn Pro Phe Gln Ala Arg Gln
 165 170 175

Val Val Glu Arg Gly Cys Gly Asp Arg Arg Ser Gly Asp Val Glu Pro
 180 185 190

Val Glu Gly Leu Gly Asp Arg Glu Gly Cys Gly Leu Glu Thr Val Gly
 195 200 205

Gly Val Gly Gly Ile Ala Gly Ser Asp Leu Gly Leu Asn Gln Arg Pro
 210 215 220

Gln Asp Leu Leu Arg Cys Pro Ala Leu Arg Leu Gly Asp Leu Gln His
 225 230 235 240

Leu Gly Gly Val Ala Ala His Arg Gly Gln Leu Gln Pro Pro Gln Arg
 245 250 255

Arg Val Lys Val Ser Ser Gln Arg Cys Arg Arg Gly Arg Cys His Arg
 260 265 270

Leu Gly Ser Gly Gly His Glu Ala Val Pro Ser Val Val Leu Ile Leu
 275 280 285

<210> 27
 <211> 1739
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(945)

<400> 27
 atg ggc tgc ctc aaa ggt ggt gtc gtc gcc aat gtt gtt gtt cca aca 48
 Met Gly Cys Leu Lys Gly Gly Val Val Ala Asn Val Val Val Pro Thr
 1 5 10 15

ccg gat tat gtg cga ttc gcg tcc cac tat ggc ttc gtt ccg gac ttc 96
 Pro Asp Tyr Val Arg Phe Ala Ser His Tyr Gly Phe Val Pro Asp Phe
 20 25 30

tgc cac ggt gcg gat ccg caa tcg aag ggc atc gtg gag aac ctc tgt 144
 Cys His Gly Ala Asp Pro Gln Ser Lys Gly Ile Val Glu Asn Leu Cys
 35 40 45

ggc tac gct cag gac gac ctt gcg gtg ccg ctg ctg acc gaa gct gcg 192
 Gly Tyr Ala Gln Asp Asp Leu Ala Val Pro Leu Leu Thr Glu Ala Ala
 50 55 60

tta gcc ggt gag cag gtc gac cta cgt gcc ctc aac gcc cag gcg caa 240
 Leu Ala Gly Glu Gln Val Asp Leu Arg Ala Leu Asn Ala Gln Ala Gln
 65 70 75 80

cta tgg tgc gcc gag gtc aat gcc acg gtc cac tcg gag atc tgc gcc	288
Leu Trp Cys Ala Glu Val Asn Ala Thr Val His Ser Glu Ile Cys Ala	
85 90 95	
gtg ccc aac gat cgc ttg gtt gac gag cgc acc gtc ttg agg gag ctg	336
Val Pro Asn Asp Arg Leu Val Asp Glu Arg Thr Val Leu Arg Glu Leu	
100 105 110	
ccc tcg ctg cgg ccg acg atc ggc tcg ggg tcg gtg cgc cgt aag gtc	384
Pro Ser Leu Arg Pro Thr Ile Gly Ser Gly Ser Val Arg Arg Lys Val	
115 120 125	
gac ggc ctc tcg tgc atc cgt tac ggc tca gct cgt tac tcg gtg cct	432
Asp Gly Leu Ser Cys Ile Arg Tyr Gly Ser Ala Arg Tyr Ser Val Pro	
130 135 140	
cag cgg ctc gtc ggt gcc acc gtg gcg gtg gtg gtc gat cat ggc gcc	480
Gln Arg Leu Val Gly Ala Thr Val Ala Val Val Val Asp His Gly Ala	
145 150 155 160	
ctg atc ctg ttg gaa cct gcg acc ggt gtg atc gtg gcc gag cac gag	528
Leu Ile Leu Leu Glu Pro Ala Thr Gly Val Ile Val Ala Glu His Glu	
165 170 175	
ctc gtc agc cca ggt gag gtg tcc atc ctc gat gaa cac tac gac gga	576
Leu Val Ser Pro Gly Glu Val Ser Ile Leu Asp Glu His Tyr Asp Gly	
180 185 190	
ccc aga ccc gca ccc tcg cgt ggt cct cgc ccg aaa acc caa gca gag	624
Pro Arg Pro Ala Pro Ser Arg Gly Pro Arg Pro Lys Thr Gln Ala Glu	
195 200 205	
aaa cga ttc tgc gca ttg gga acc gaa gcg cag cag ttc ctc gtc ggt	672
Lys Arg Phe Cys Ala Leu Gly Thr Glu Ala Gln Gln Phe Leu Val Gly	
210 215 220	
gct gct gcg atc ggc aac acc cga ctg aaa tcc gaa ctc gac att ctg	720
Ala Ala Ala Ile Gly Asn Thr Arg Leu Lys Ser Glu Leu Asp Ile Leu	
225 230 235 240	
ctc ggc ctt ggc gcc gcc cac ggc gaa cag gct ttg att gac gcg ctg	768
Leu Gly Leu Gly Ala Ala His Gly Glu Gln Ala Leu Ile Asp Ala Leu	
245 250 255	
cgc cgg gcg gtt gcg ttt cgc cgg ttc cgc gct gcc gac gtg cgc tcg	816
Arg Arg Ala Val Ala Phe Arg Arg Phe Arg Ala Ala Asp Val Arg Ser	
260 265 270	
atc ctg gcc gcc ggc gcc ggc acc cca caa ccc cgc ccc gcc ggc gac	864
Ile Leu Ala Ala Gly Ala Gly Thr Pro Gln Pro Arg Pro Ala Gly Asp	
275 280 285	
gca ctc gtg ctc gat ctg ccc acc gtc gag acc cgc tcg ttg gag gcc	912
Ala Leu Val Leu Asp Leu Pro Thr Val Glu Thr Arg Ser Leu Glu Ala	
290 295 300	
tac aag atc aac acc acc gac ggg acg gcc tca tgaccaccgc tgccaagccg	965
Tyr Lys Ile Asn Thr Thr Asp Gly Thr Ala Ser	
305 310 315	
gtggcaccgt cctcggcggc accgctggt gctgaccttg acgcggcgct gcggcggttg	1025

aagctggcca cggtagcgccg caacgccgcc gaggtgttgc aagtcgcca gacgcaacgc 1085
tggacaccgg aggagatcct gcggacgttg gttgaggccg agatcgctgc ccgcatgcc 1145
tccaacaccg ccaaccgtct caaggccgca gccttcccgg tcaccaagac cctcgacggg 1205
ttcgacgtca ccggatcgtc gatcaccgca gccacgttcg actacctgtc gagcctggaa 1265
tggattcggg cacaacagaa cctggcggtc attggcccac ctggtacggg caaaagtcac 1325
ctgctcatcg gctgcgggca cgctgccgtc cacgccgat tcaaagtcg ctacttcacc 1385
gccgccgacc tgatcgaggt cctctaccgc ggcttgccg acaacaccgt cggcaagatc 1445
atcgacaccc tgctccgctc ggatctggtc atcttgacg agatcggctt cggccgctc 1505
gacgacaccg ggactcaact gttgttccgg ctctgtggtg ccggctacga gcgccgctcc 1565
ctggccatcg cctcgcattg gcccttcgaa caatgggggc gattctgtcc cgagcacacc 1625
accgccgcca gcctcctcga tcggctgctg caccacgcca gcctcgtct cacctccggc 1685
gagtcctacc ggatgcgcca cgccgaccac aagaaggag ccgccaagaa ttag 1739

<210> 28

<211> 315

<212> PRT

<213> Mycobacterium

<400> 28

Met Gly Cys Leu Lys Gly Gly Val Val Ala Asn Val Val Val Pro Thr
1 5 10 15

Pro Asp Tyr Val Arg Phe Ala Ser His Tyr Gly Phe Val Pro Asp Phe
20 25 30

Cys His Gly Ala Asp Pro Gln Ser Lys Gly Ile Val Glu Asn Leu Cys
35 40 45

Gly Tyr Ala Gln Asp Asp Leu Ala Val Pro Leu Leu Thr Glu Ala Ala
50 55 60

Leu Ala Gly Glu Gln Val Asp Leu Arg Ala Leu Asn Ala Gln Ala Gln
65 70 75 80

Leu Trp Cys Ala Glu Val Asn Ala Thr Val His Ser Glu Ile Cys Ala
85 90 95

Val Pro Asn Asp Arg Leu Val Asp Glu Arg Thr Val Leu Arg Glu Leu
100 105 110

Pro Ser Leu Arg Pro Thr Ile Gly Ser Gly Ser Val Arg Arg Lys Val
115 120 125

Asp Gly Leu Ser Cys Ile Arg Tyr Gly Ser Ala Arg Tyr Ser Val Pro
130 135 140

Gln Arg Leu Val Gly Ala Thr Val Ala Val Val Val Asp His Gly Ala
145 150 155 160

Leu Ile Leu Leu Glu Pro^{*} Ala Thr Gly Val Ile Val Ala Glu His Glu
 165 170 175
 Leu Val Ser Pro Gly Glu Val Ser Ile Leu Asp Glu His Tyr Asp Gly
 180 185 190
 Pro Arg Pro Ala Pro Ser Arg Gly Pro Arg Pro Lys Thr Gln Ala Glu
 195 200 205
 Lys Arg Phe Cys Ala Leu Gly Thr Glu Ala Gln Gln Phe Leu Val Gly
 210 215 220
 Ala Ala Ala Ile Gly Asn Thr Arg Leu Lys Ser Glu Leu Asp Ile Leu
 225 230 235 240
 Leu Gly Leu Gly Ala Ala His Gly Glu Gln Ala Leu Ile Asp Ala Leu
 245 250 255
 Arg Arg Ala Val Ala Phe Arg Arg Phe Arg Ala Ala Asp Val Arg Ser
 260 265 270
 Ile Leu Ala Ala Gly Ala Gly Thr Pro Gln Pro Arg Pro Ala Gly Asp
 275 280 285
 Ala Leu Val Leu Asp Leu Pro Thr Val Glu Thr Arg Ser Leu Glu Ala
 290 295 300
 Tyr Lys Ile Asn Thr Thr Asp Gly Thr Ala Ser
 305 310 315

<210> 29

<211> 264

<212> PRT

<213> Mycobacterium

<220>

<221> DOMAIN

<222> (1)..(264)

<223> amino acid sequence is encoded by nucleotides
945-1736 of SEQ ID NO:27

<400> 29

Met Thr Thr Ala Ala Lys Pro Val Ala Pro Ser Ser Ala Ala Pro Leu
 1 5 10 15
 Ala Ala Asp Leu Asp Ala Ala Leu Arg Arg Leu Lys Leu Ala Thr Val
 20 25 30
 Arg Arg Asn Ala Ala Glu Val Leu Gln Val Ala Lys Thr Gln Arg Trp
 35 40 45
 Thr Pro Glu Glu Ile Leu Arg Thr Leu Val Glu Ala Glu Ile Ala Ala
 50 55 60
 Arg Asp Ala Ser Asn Thr Ala Asn Arg Leu Lys Ala Ala Ala Phe Pro
 65 70 75 80
 Val Thr Lys Thr Leu Asp Gly Phe Asp Val Thr Gly Ser Ser Ile Thr
 85 90 95

Ala Ala Thr Phe Asp Tyr Leu Ser Ser Leu Glu Trp Ile Arg Ala Gln
100 105 110

Gln Asn Leu Ala Val Ile Gly Pro Pro Gly Thr Gly Lys Ser His Leu
115 120 125

Leu Ile Gly Cys Gly His Ala Ala Val His Ala Gly Phe Lys Val Arg
130 135 140

Tyr Phe Thr Ala Ala Asp Leu Ile Glu Val Leu Tyr Arg Gly Leu Ala
145 150 155 160

Asp Asn Thr Val Gly Lys Ile Ile Asp Thr Leu Leu Arg Ala Asp Leu
165 170 175

Val Ile Leu Asp Glu Ile Gly Phe Ala Pro Leu Asp Asp Thr Gly Thr
180 185 190

Gln Leu Leu Phe Arg Leu Val Ala Ala Gly Tyr Glu Arg Arg Ser Leu
195 200 205

Ala Ile Ala Ser His Trp Pro Phe Glu Gln Trp Gly Arg Phe Leu Pro
210 215 220

Glu His Thr Thr Ala Ala Ser Ile Leu Asp Arg Leu Leu His His Ala
225 230 235 240

Ser Ile Val Val Thr Ser Gly Glu Ser Tyr Arg Met Arg His Ala Asp
245 250 255

His Lys Lys Gly Ala Ala Lys Asn
260

<210> 30
<211> 789
<212> DNA
<213> Mycobacterium

<220>
<221> CDS
<222> (1)..(786)

<400> 30
gtg acg tct gct ccg acc gtc tcg gtg ata acg atc tcg ttc aac gac 48
Met Thr Ser Ala Pro Thr Val Ser Val Ile Thr Ile Ser Phe Asn Asp
1 5 10 15

ctc gac ggg ttg cag cgc acg gtg.aaa agt gtg cgg gcg caa cgc tac 96
Leu Asp Gly Leu Gln Arg Thr Val Lys Ser Val Arg Ala Gln Arg Tyr
20 25 30

cgg gga cgc atc gag cac atc gta atc gac ggt ggc agc ggc gac gac 144
Arg Gly Arg Ile Glu His Ile Val Ile Asp Gly Gly Ser Gly Asp Asp
35 40 45

gtg gtg gca tac ctg tcc ggg tgt gaa cca ggc ttc gcg tat tgg cag 192
Val Val Ala Tyr Leu Ser Gly Cys Glu Pro Gly Phe Ala Tyr Trp Gln
50 55 60

tcc gag ccc gac ggc ggg. cgg tac gac gcg atg aac cag ggc atc gcg Ser Glu Pro Asp Gly Gly Arg Tyr Asp Ala Met Asn Gln Gly Ile Ala 65 70 75 80	240
cac gca tcg ggt gat ctg ttg tgg ttc ttg cac tcc gcc gat cgt ttt His Ala Ser Gly Asp Leu Leu Trp Phe Leu His Ser Ala Asp Arg Phe 85 90 95	288
tcc ggg ccc gac gtg gta gcc cag gcc gtg gag gcg cta tcc ggc aag Ser Gly Pro Asp Val Val Ala Gln Ala Val Glu Ala Leu Ser Gly Lys 100 105 110	336
gga ccg gtg tcc gaa ttg tgg ggc ttc ggg atg gat cgt ctc gtc ggg Gly Pro Val Ser Glu Leu Trp Gly Phe Gly Met Asp Arg Leu Val Gly 115 120 125	384
ctc gat cgg gtg cgc ggc ccg ata cct ttc agc ctg cgc aaa ttc ctg Leu Asp Arg Val Arg Gly Pro Ile Pro Phe Ser Leu Arg Lys Phe Leu 130 135 140	432
gcc ggc aag cag gtt gtt ccg cat caa gca tcg ttc ttc gga tca tcg Ala Gly Lys Gln Val Val Pro His Gln Ala Ser Phe Phe Gly Ser Ser 145 150 155 160	480
ctg gtg gcc aag atc ggt ggc tac gac ctt gat ttc ggg atc gcc gcc Leu Val Ala Lys Ile Gly Gly Tyr Asp Leu Asp Phe Gly Ile Ala Ala 165 170 175	528
gac cag gaa ttc ata ttg ccg gcc gcg ctg gta tgc gag ccg gtc acg Asp Gln Glu Phe Ile Leu Arg Ala Ala Leu Val Cys Glu Pro Val Thr 180 185 190	576
att ccg tgt gtg ctg tgc gag ttc gac acc acg ggc gtc ggc tcg cac Ile Arg Cys Val Leu Cys Glu Phe Asp Thr Thr Gly Val Gly Ser His 195 200 205	624
ccg gaa cca agc gcg gtc ttc ggt gat ctg cgc cgc atg ggc gac ctt Arg Glu Pro Ser Ala Val Phe Gly Asp Leu Arg Arg Met Gly Asp Leu 210 215 220	672
cat cgc cgc tac ccg ttc ggg gga agg cga ata tca cat gcc tac cta His Arg Arg Tyr Pro Phe Gly Gly Arg Arg Ile Ser His Ala Tyr Leu 225 230 235 240	720
cgc ggc ccg gag ttc tac gcc tac aac agt cga ttc tgg gaa aac gtc Arg Gly Arg Glu Phe Tyr Ala Tyr Asn Ser Arg Phe Trp Glu Asn Val 245 250 255	768
ttc acg cga atg tcg aaa tag Phe Thr Arg Met Ser Lys 260	789

<210> 31
 <211> 262
 <212> PRT
 <213> Mycobacterium

<400> 31
 Met Thr Ser Ala Pro Thr Val Ser Val Ile Thr Ile Ser Phe Asn Asp
 1 5 10 15

Leu Asp Gly Leu Gln Arg Thr Val Lys Ser Val Arg Ala Gln Arg Tyr
 20 25 30
 Arg Gly Arg Ile Glu His Ile Val Ile Asp Gly Gly Ser Gly Asp Asp
 35 40 45
 Val Val Ala Tyr Leu Ser Gly Cys Glu Pro Gly Phe Ala Tyr Trp Gln
 50 55 60
 Ser Glu Pro Asp Gly Gly Arg Tyr Asp Ala Met Asn Gln Gly Ile Ala
 65 70 75 80
 His Ala Ser Gly Asp Leu Leu Trp Phe Leu His Ser Ala Asp Arg Phe
 85 90 95
 Ser Gly Pro Asp Val Val Ala Gln Ala Val Glu Ala Leu Ser Gly Lys
 100 105 110
 Gly Pro Val Ser Glu Leu Trp Gly Phe Gly Met Asp Arg Leu Val Gly
 115 120 125
 Leu Asp Arg Val Arg Gly Pro Ile Pro Phe Ser Leu Arg Lys Phe Leu
 130 135 140
 Ala Gly Lys Gln Val Val Pro His Gln Ala Ser Phe Phe Gly Ser Ser
 145 150 155 160
 Leu Val Ala Lys Ile Gly Gly Tyr Asp Leu Asp Phe Gly Ile Ala Ala
 165 170 175
 Asp Gln Glu Phe Ile Leu Arg Ala Ala Leu Val Cys Glu Pro Val Thr
 180 185 190
 Ile Arg Cys Val Leu Cys Glu Phe Asp Thr Thr Gly Val Gly Ser His
 195 200 205
 Arg Glu Pro Ser Ala Val Phe Gly Asp Leu Arg Arg Met Gly Asp Leu
 210 215 220
 His Arg Arg Tyr Pro Phe Gly Gly Arg Arg Ile Ser His Ala Tyr Leu
 225 230 235 240
 Arg Gly Arg Glu Phe Tyr Ala Tyr Asn Ser Arg Phe Trp Glu Asn Val
 245 250 255
 Phe Thr Arg Met Ser Lys
 260

<210> 32
 <211> 1023
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(1020)

<400> 32
 gtg aag cga gcg ctc atc acc gga atc acc ggc cag gac ggc tcg tat 48
 Met Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr
 1 5 10 15

 ctc gcc gaa ctg ctg ctg gcc aag ggg tat gag gtt cac ggg ctc atc 96
 Leu Ala Glu Leu Leu Leu Ala Lys Gly Tyr Glu Val His Gly Leu Ile
 20 25 30

 cgg cgc gct tcg acg ttc aac acc tcg cgg atc gat cac ctc tac gtc 144
 Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val
 35 40 45

 gac ccg cac caa ccg ggc gcg cgg ctg ttt ctg cac tat ggt gac ctg 192
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Gly Asp Leu
 50 55 60

 atc gac gga acc cgg ttg gtg acc ctg ctg agc acc atc gaa ccc gac 240
 Ile Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Thr Ile Glu Pro Asp
 65 70 75 80

 gag gtg tac aac ctg gcg gcg cag tca cac gtg cgg gtg agc ttc gac 288
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp
 85 90 95

 gaa ccc gtg cac acc ggt gac acc acc ggc atg gga tcc atg cga ctg 336
 Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Met Arg Leu
 100 105 110

 ctg gaa gcc gtt cgg ctc tct cgg gtg cac tgc cgc ttc tat cag gcg 384
 Leu Glu Ala Val Arg Leu Ser Arg Val His Cys Arg Phe Tyr Gln Ala
 115 120 125

 tcc tcg tcg gag atg ttc ggc gcc tcg ccg cca ccg cag aac gag ctg 432
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Leu
 130 135 140

 acg ccg ttc tac ccg cgg tca ccg tat ggc gcc gcc aag gtc tat tcg 480
 Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Tyr Ser
 145 150 155 160

 tac tgg gcg acc cgc aat tat cgc gaa gcg tac gga ttg ttc gcc gtc 528
 Tyr Trp Ala Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val
 165 170 175

 aac ggc atc ttg ttc aat cac gaa tca ccg cgg cgc ggt gag acg ttc 576
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe
 180 185 190

 gtg acc cga aag atc acc agg gcc gtg gca cgc atc aag gcc ggt atc 624
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Lys Ala Gly Ile
 195 200 205

 cag tcc gag gtc tat atg ggc aat ctg gat gcg gtc cgc gac tgg ggg 672
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Val Arg Asp Trp Gly
 210 215 220

 tac gcg ccc gaa tac gtc gaa ggc atg tgg cgg atg ctg cag acc gac 720
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Thr Asp
 225 230 235 240

gag ccc gac gac ttc gtt^{*} ttg geg acc ggg cgc ggt ttc acc gtg cgt 768
 Glu Pro Asp Asp Phe Val Leu Ala Thr Gly Arg Gly Phe Thr Val Arg
 245 250 255

gag ttc gcg cgg gcc gcg ttc gag cat gcc ggt ttg gac tgg cag cag 816
 Glu Phe Ala Arg Ala Ala Phe Glu His Ala Gly Leu Asp Trp Gln Gln
 260 265 270

tac gtg aaa ttc gac caa cgc tat ctg cgg ccc acc gag gtg gat tcg 864
 Tyr Val Lys Phe Asp Gln Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser
 275 280 285

ctg atc ggc gac gcg acc aag gct gcc gaa ttg ctg ggc tgg agg gct 912
 Leu Ile Gly Asp Ala Thr Lys Ala Ala Glu Leu Leu Gly Trp Arg Ala
 290 295 300

tcg gtg cac act gac gag ttg gct cgg atc atg gtc gac gcg gac atg 960
 Ser Val His Thr Asp Glu Leu Ala Arg Ile Met Val Asp Ala Asp Met
 305 310 315 320

gcg gcg ctg gag tgc gaa ggc aag ccg tgg atc gac aag ccg atg atc 1008
 Ala Ala Leu Glu Cys Glu Gly Lys Pro Trp Ile Asp Lys Pro Met Ile
 325 330 335

gcc ggc cgg aca tga 1023
 Ala Gly Arg Thr
 340

<210> 33
 <211> 340
 <212> PRT
 <213> Mycobacterium

<400> 33
 Met Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr
 1 5 10 15

Leu Ala Glu Leu Leu Leu Ala Lys Gly Tyr Glu Val His Gly Leu Ile
 20 25 30

Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val
 35 40 45

Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Gly Asp Leu
 50 55 60

Ile Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Thr Ile Glu Pro Asp
 65 70 75 80

Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp
 85 90 95

Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Met Arg Leu
 100 105 110

Leu Glu Ala Val Arg Leu Ser Arg Val His Cys Arg Phe Tyr Gln Ala
 115 120 125

Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Leu
 130 135 140

Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Tyr Ser
 145 150 155 160
 Tyr Trp Ala Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val
 165 170 175
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe
 180 185 190
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Lys Ala Gly Ile
 195 200 205
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Val Arg Asp Trp Gly
 210 215 220
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Thr Asp
 225 230 235 240
 Glu Pro Asp Asp Phe Val Leu Ala Thr Gly Arg Gly Phe Thr Val Arg
 245 250 255
 Glu Phe Ala Arg Ala Ala Phe Glu His Ala Gly Leu Asp Trp Gln Gln
 260 265 270
 Tyr Val Lys Phe Asp Gln Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser
 275 280 285
 Leu Ile Gly Asp Ala Thr Lys Ala Ala Glu Leu Leu Gly Trp Arg Ala
 290 295 300
 Ser Val His Thr Asp Glu Leu Ala Arg Ile Met Val Asp Ala Asp Met
 305 310 315 320
 Ala Ala Leu Glu Cys Glu Gly Lys Pro Trp Ile Asp Lys Pro Met Ile
 325 330 335
 Ala Gly Arg Thr
 340

<210> 34
 <211> 732
 <212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(729)

<400> 34
 atg agg ctg gcc cgt cgc gct cgg aac atc ttg cgt cgc aac ggc atc 48
 Met Arg Leu Ala Arg Arg Ala Arg Asn Ile Leu Arg Arg Asn Gly Ile
 1 5 10 15
 gag gtg tcg cgc tac ttt gcc gaa ctg gac tgg gaa cgc aat ttc ttg 96
 Glu Val Ser Arg Tyr Phe Ala Glu Leu Asp Trp Glu Arg Asn Phe Leu
 20 25 30

cgc caa ctg caa tcg cat.cgg gtc agt gcc gtg ctc gat gtc ggg gcc	144
Arg Gln Leu Gln Ser His Arg Val Ser Ala Val Leu Asp Val Gly Ala	
35 40 45	
aat tcg ggg cag tac gcc agg ggt ctg cgc ggc gcg ggc ttc gcg ggc	192
Asn Ser Gly Gln Tyr Ala Arg Gly Leu Arg Gly Ala Gly Phe Ala Gly	
50 55 60	
cgc atc gtc tcg ttc gag ccg ctg ccc ggg ccc ttt gcc gtc ttg cag	240
Arg Ile Val Ser Phe Glu Pro Leu Pro Gly Pro Phe Ala Val Leu Gln	
65 70 75 80	
cgc agc gcc tcc acg gac ccg ttg tgg gaa tgc cgg cgc tgt gcg ctg	288
Arg Ser Ala Ser Thr Asp Pro Leu Trp Glu Cys Arg Arg Cys Ala Leu	
85 90 95	
ggc gat gtc gat gga acc atc tcg atc aac gtc gcc ggc aac gag ggc	336
Gly Asp Val Asp Gly Thr Ile Ser Ile Asn Val Ala Gly Asn Glu Gly	
100 105 110	
gcc agc agt tcc gtc ttg ccg atg ttg aaa cga cat cag gac gcc ttt	384
Ala Ser Ser Ser Val Leu Pro Met Leu Lys Arg His Gln Asp Ala Phe	
115 120 125	
cca cca gcc aac tac gtg ggc gcc caa cgg gtg ccg ata cat cga ctc	432
Pro Pro Ala Asn Tyr Val Gly Ala Gln Arg Val Pro Ile His Arg Leu	
130 135 140	
gat tcc gtg gct gca gac gtt ctg cgg ccc aac gat att gcg ttc ttg	480
Asp Ser Val Ala Ala Asp Val Leu Arg Pro Asn Asp Ile Ala Phe Leu	
145 150 155 160	
aag atc gac gtt caa gga ttc gag aag cag gtg atc gcg ggt ggc gat	528
Lys Ile Asp Val Gln Gly Phe Glu Lys Gln Val Ile Ala Gly Gly Asp	
165 170 175	
tca acg gtg cac gac cga tgc gtc ggc atg cag ctc gag ctg tct ttc	576
Ser Thr Val His Asp Arg Cys Val Gly Met Gln Leu Glu Leu Ser Phe	
180 185 190	
cag ccg ttg tac gag ggt ggc atg ctc atc cgc gag gcg ctc gat ctc	624
Gln Pro Leu Tyr Glu Gly Gly Met Leu Ile Arg Glu Ala Leu Asp Leu	
195 200 205	
gtg gat tcg ttg ggc ttt acg ctc tcg gga ttg caa ccc ggt ttc acc	672
Val Asp Ser Leu Gly Phe Thr Leu Ser Gly Leu Gln Pro Gly Phe Thr	
210 215 220	
gac ccc cgc aac ggt cga atg ctg cag gcc gat ggc atc ttc ttc cgg	720
Asp Pro Arg Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg	
225 230 235 240	
ggc agc gat tga	732
Gly Ser Asp	

<210> 35

<211> 243

<212> PRT

<213> Mycobacterium

<400> 35

```

Met Arg Leu Ala Arg Arg Ala Arg Asn Ile Leu Arg Arg Asn Gly Ile
 1           5           10           15

Glu Val Ser Arg Tyr Phe Ala Glu Leu Asp Trp Glu Arg Asn Phe Leu
          20           25           30

Arg Gln Leu Gln Ser His Arg Val Ser Ala Val Leu Asp Val Gly Ala
          35           40           45

Asn Ser Gly Gln Tyr Ala Arg Gly Leu Arg Gly Ala Gly Phe Ala Gly
          50           55           60

Arg Ile Val Ser Phe Glu Pro Leu Pro Gly Pro Phe Ala Val Leu Gln
          65           70           75           80

Arg Ser Ala Ser Thr Asp Pro Leu Trp Glu Cys Arg Arg Cys Ala Leu
          85           90           95

Gly Asp Val Asp Gly Thr Ile Ser Ile Asn Val Ala Gly Asn Glu Gly
          100          105          110

Ala Ser Ser Ser Val Leu Pro Met Leu Lys Arg His Gln Asp Ala Phe
          115          120          125

Pro Pro Ala Asn Tyr Val Gly Ala Gln Arg Val Pro Ile His Arg Leu
          130          135          140

Asp Ser Val Ala Ala Asp Val Leu Arg Pro Asn Asp Ile Ala Phe Leu
          145          150          155          160

Lys Ile Asp Val Gln Gly Phe Glu Lys Gln Val Ile Ala Gly Gly Asp
          165          170          175

Ser Thr Val His Asp Arg Cys Val Gly Met Gln Leu Glu Leu Ser Phe
          180          185          190

Gln Pro Leu Tyr Glu Gly Gly Met Leu Ile Arg Glu Ala Leu Asp Leu
          195          200          205

Val Asp Ser Leu Gly Phe Thr Leu Ser Gly Leu Gln Pro Gly Phe Thr
          210          215          220

Asp Pro Arg Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg
          225          230          235          240

Gly Ser Asp

```

<210> 36

<211> 732

<212> DNA

<213> Mycobacterium

<220>

<221> CDS

<222> (1)..(729)

<400> 36
 gtg aaa tcg ttg aaa ctg gct cgt ttc atc gcg cgt agc gcc gcc ttc 48
 Met Lys Ser Leu Lys Leu Ala Arg Phe Ile Ala Arg Ser Ala Ala Phe
 1 5 10 15

gag gtt tcg cgc cgc tat tct gag cga gac ctg aag cac cag ttt gtg 96
 Glu Val Ser Arg Arg Tyr Ser Glu Arg Asp Leu Lys His Gln Phe Val
 20 25 30

aag caa ctc aaa tcg cgt cgg gta gat gtc gtt ttc gat gtc gcc gcc 144
 Lys Gln Leu Lys Ser Arg Arg Val Asp Val Val Phe Asp Val Gly Ala
 35 40 45

aac tca gga caa tac gcc gcc gcc ctc cgc cga gca gca tat aag gcc 192
 Asn Ser Gly Gln Tyr Ala Ala Gly Leu Arg Arg Ala Ala Tyr Lys Gly
 50 55 60

cgc att gtc tcg ttc gaa ccg cta tcc gga ccg ttt acg atc ttg gaa 240
 Arg Ile Val Ser Phe Glu Pro Leu Ser Gly Pro Phe Thr Ile Leu Glu
 65 70 75 80

agc aaa gcg tca acg gat cca ctt tgg gat tgc cgg cag cat gcg ttg 288
 Ser Lys Ala Ser Thr Asp Pro Leu Trp Asp Cys Arg Gln His Ala Leu
 85 90 95

ggc gat tct gat gga acg gtt acg atc aat atc gca gga aac gcc ggt 336
 Gly Asp Ser Asp Gly Thr Val Thr Ile Asn Ile Ala Gly Asn Ala Gly
 100 105 110

cag agc agt tcc gtc ttg ccc atg ctg aaa agt cat cag aac gct ttt 384
 Gln Ser Ser Ser Val Leu Pro Met Leu Lys Ser His Gln Asn Ala Phe
 115 120 125

ccc ccg gca aac tat gtc ggt acc caa gag gcg tcc ata cat cga ctt 432
 Pro Pro Ala Asn Tyr Val Gly Thr Gln Glu Ala Ser Ile His Arg Leu
 130 135 140

gat tcc gtg gcg cca gaa ttt cta ggc atg aac ggt gtc gct ttt ctc 480
 Asp Ser Val Ala Pro Glu Phe Leu Gly Met Asn Gly Val Ala Phe Leu
 145 150 155 160

aag gtc gac gtt caa gcc ttt gaa aag cag gtg ctc gcc ggg gcc aaa 528
 Lys Val Asp Val Gln Gly Phe Glu Lys Gln Val Leu Ala Gly Gly Lys
 165 170 175

tca acc ata gat gac cat tgc gtc gcc atg caa ctc gaa ctg tcc ttc 576
 Ser Thr Ile Asp Asp His Cys Val Gly Met Gln Leu Glu Leu Ser Phe
 180 185 190

ctg ccg ttg tac gaa ggt gcc atg ctc att cct gaa gcc ctc gat ctc 624
 Leu Pro Leu Tyr Glu Gly Gly Met Leu Ile Pro Glu Ala Leu Asp Leu
 195 200 205

gtg tat tcc ttg gcc ttc acg ttg acg gga ttg ctg cct tgt ttc att 672
 Val Tyr Ser Leu Gly Phe Thr Leu Thr Gly Leu Leu Pro Cys Phe Ile
 210 215 220

gat gca aat aat ggt cga atg ttg cag gcc gac gcc atc ttt ttc cgc 720
 Asp Ala Asn Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg
 225 230 235 240

gag gac gat tga
Glu Asp Asp

<210> 37
<211> 243
<212> PRT
<213> Mycobacterium

<400> 37
Met Lys Ser Leu Lys Leu Ala Arg Phe Ile Ala Arg Ser Ala Ala Phe
1 5 10 15
Glu Val Ser Arg Arg Tyr Ser Glu Arg Asp Leu Lys His Gln Phe Val
20 25 30
Lys Gln Leu Lys Ser Arg Arg Val Asp Val Val Phe Asp Val Gly Ala
35 40 45
Asn Ser Gly Gln Tyr Ala Ala Gly Leu Arg Arg Ala Ala Tyr Lys Gly
50 55 60
Arg Ile Val Ser Phe Glu Pro Leu Ser Gly Pro Phe Thr Ile Leu Glu
65 70 75 80
Ser Lys Ala Ser Thr Asp Pro Leu Trp Asp Cys Arg Gln His Ala Leu
85 90 95
Gly Asp Ser Asp Gly Thr Val Thr Ile Asn Ile Ala Gly Asn Ala Gly
100 105 110
Gln Ser Ser Ser Val Leu Pro Met Leu Lys Ser His Gln Asn Ala Phe
115 120 125
Pro Pro Ala Asn Tyr Val Gly Thr Gln Glu Ala Ser Ile His Arg Leu
130 135 140
Asp Ser Val Ala Pro Glu Phe Leu Gly Met Asn Gly Val Ala Phe Leu
145 150 155 160
Lys Val Asp Val Gln Gly Phe Glu Lys Gln Val Leu Ala Gly Gly Lys
165 170 175
Ser Thr Ile Asp Asp His Cys Val Gly Met Gln Leu Glu Leu Ser Phe
180 185 190
Leu Pro Leu Tyr Glu Gly Gly Met Leu Ile Pro Glu Ala Leu Asp Leu
195 200 205
Val Tyr Ser Leu Gly Phe Thr Leu Thr Gly Leu Leu Pro Cys Phe Ile
210 215 220
Asp Ala Asn Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg
225 230 235 240
Glu Asp Asp

<210> 38
<211> 828

<212> DNA
 <213> Mycobacterium

<220>
 <221> CDS
 <222> (1)..(825)

<400> 38
 atg gtg cag acg aaa cga tac gcc ggc ttg acc gca gct aac aca aag 48
 Met Val Gln Thr Lys Arg Tyr Ala Gly Leu Thr Ala Ala Asn Thr Lys
 1 5 10 15

aaa gtc gcc atg gcc gca cca atg ttt tcg atc atc atc ccc acc ttg 96
 Lys Val Ala Met Ala Ala Pro Met Phe Ser Ile Ile Ile Pro Thr Leu
 20 25 30

aac gtg gct gcg gta ttg cct gcc tgc ctc gac agc atc gcc cgt cag 144
 Asn Val Ala Ala Val Leu Pro Ala Cys Leu Asp Ser Ile Ala Arg Gln
 35 40 45

acc tgc ggt gac ttc gag ctg gta ctg gtc gac ggc ggc tcg acg gac 192
 Thr Cys Gly Asp Phe Glu Leu Val Leu Val Asp Gly Gly Ser Thr Asp
 50 55 60

gaa acc ctc gac atc gcc aac att ttc gcc ccc aac ctc ggc gag cgg 240
 Glu Thr Leu Asp Ile Ala Asn Ile Phe Ala Pro Asn Leu Gly Glu Arg
 65 70 75 80

ttg atc att cat cgc gac acc gac cag ggc gtc tac gac gcc atg aac 288
 Leu Ile Ile His Arg Asp Thr Asp Gln Gly Val Tyr Asp Ala Met Asn
 85 90 95

cgc ggc gtg gac ctg gcc acc gga acg tgg ttg ctc ttt ctg ggc gcg 336
 Arg Gly Val Asp Leu Ala Thr Gly Thr Trp Leu Leu Phe Leu Gly Ala
 100 105 110

gac gac agc ctg tac gag gct gac acc ctg gcg cgg gtg gcc gcc ttc 384
 Asp Asp Ser Leu Tyr Glu Ala Asp Thr Leu Ala Arg Val Ala Ala Phe
 115 120 125

att ggc gaa cac gag ccc agc gat ctg gta tat ggc gac gtg atc atg 432
 Ile Gly Glu His Glu Pro Ser Asp Leu Val Tyr Gly Asp Val Ile Met
 130 135 140

cgc tca acc aat ttc cgc tgg ggt ggc gcc ttc gac ctc gac cgt ctg 480
 Arg Ser Thr Asn Phe Arg Trp Gly Gly Ala Phe Asp Leu Asp Arg Leu
 145 150 155 160

ttg ttc aag cgc aac atc tgc cat cag gcg atc ttc tac cgc cgc gga 528
 Leu Phe Lys Arg Asn Ile Cys His Gln Ala Ile Phe Tyr Arg Arg Gly
 165 170 175

ctc ttc ggc acc atc ggt ccc tac aac ctc cgc tac cgg gtc ctg gcc 576
 Leu Phe Gly Thr Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Leu Ala
 180 185 190

gac tgg gac ttc aat att cgc tgc ttt tcc aac cca gcg ctc gtc acc 624
 Asp Trp Asp Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Val Thr
 195 200 205

cgc tac atg caç gtg gtc gtt gca agc tac aac gaa ttc ggc ggg ctc 672
 Arg Tyr Met His Val Val Val Ala Ser Tyr Asn Glu Phe Gly Gly Leu
 210 215 220
 agc aat acg atc gtc gac aag gag ttt ttg aag cgg ctg ccg atg tcc 720
 Ser Asn Thr Ile Val Asp Lys Glu Phe Leu Lys Arg Leu Pro Met Ser
 225 230 235 240
 acg aga ctc ggc ata agg ctg gtc ata gtt ctg gtg cgc agg tgg cca 768
 Thr Arg Leu Gly Ile Arg Leu Val Ile Val Leu Val Arg Arg Trp Pro
 245 250 255
 aag gtg atc agc agg gcc atg gta atg cgc acc gtc att tct tgg cgg 816
 Lys Val Ile Ser Arg Ala Met Val Met Arg Thr Val Ile Ser Trp Arg
 260 265 270
 cgc cga cgt tag 828
 Arg Arg
 275

<210> 39
 <211> 275
 <212> PRT
 <213> Mycobacterium

<400> 39
 Met Val Gln Thr Lys Arg Tyr Ala Gly Leu Thr Ala Ala Asn Thr Lys
 1 5 10 15
 Lys Val Ala Met Ala Ala Pro Met Phe Ser Ile Ile Ile Pro Thr Leu
 20 25 30
 Asn Val Ala Ala Val Leu Pro Ala Cys Leu Asp Ser Ile Ala Arg Gln
 35 40 45
 Thr Cys Gly Asp Phe Glu Leu Val Leu Val Asp Gly Gly Ser Thr Asp
 50 55 60
 Glu Thr Leu Asp Ile Ala Asn Ile Phe Ala Pro Asn Leu Gly Glu Arg
 65 70 75 80
 Leu Ile Ile His Arg Asp Thr Asp Gln Gly Val Tyr Asp Ala Met Asn
 85 90 95
 Arg Gly Val Asp Leu Ala Thr Gly Thr Trp Leu Leu Phe Leu Gly Ala
 100 105 110
 Asp Asp Ser Leu Tyr Glu Ala Asp Thr Leu Ala Arg Val Ala Ala Phe
 115 120 125
 Ile Gly Glu His Glu Pro Ser Asp Leu Val Tyr Gly Asp Val Ile Met
 130 135 140
 Arg Ser Thr Asn Phe Arg Trp Gly Gly Ala Phe Asp Leu Asp Arg Leu
 145 150 155 160
 Leu Phe Lys Arg Asn Ile Cys His Gln Ala Ile Phe Tyr Arg Arg Gly
 165 170 175

Leu Phe Gly Thr Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Leu Ala
 180 185 190
 Asp Trp Asp Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Val Thr
 195 200 205
 Arg Tyr Met His Val Val Val Ala Ser Tyr Asn Glu Phe Gly Gly Leu
 210 215 220
 Ser Asn Thr Ile Val Asp Lys Glu Phe Leu Lys Arg Leu Pro Met Ser
 225 230 235 240
 Thr Arg Leu Gly Ile Arg Leu Val Ile Val Leu Val Arg Arg Trp Pro
 245 250 255
 Lys Val Ile Ser Arg Ala Met Val Met Arg Thr Val Ile Ser Trp Arg
 260 265 270
 Arg Arg Arg
 275

<210> 40
 <211> 24
 <212> DNA
 <213> Mycobacterium

<400> 40
 gatgccgtga ggaggtaaag ctgc

24

<210> 41
 <211> 24
 <212> DNA
 <213> Mycobacterium

<400> 41
 gatacggctc ttgaatcctg cacg

24